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Listing first 45 summaries
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                                                                                                       1834
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Comp
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ALIGNMENTS

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                                       Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
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N-PSDB; AAF29014.
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to Lyme disease
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Claim 43;

Page 78-79; 160pp; English.

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                        (UYNY ) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
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Chimeric - Borrelia
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                                                                                                     WO200078966-A1.
                                                                                                                              Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick
                                                                                                                                                 Borrelia sp chimeric ospC protein SEQ ID NO: 60.
                                                                                                                                                                       03-APR-2001 (first entry)
                                                                                                                                                                                                                        2728
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                                                                                                                                                                                                    AAB62728 standard; Protein; 398
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Best Local
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100.0%; Pr
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Pred. No. 3.2e-119;
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Gomes-Solecki M;
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RESULT
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Chimeric - Borrelia sp.
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Best Local Simi
Matches 373;
                                                                                               Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compositions of OspC polypeptides from strains of Borrelia which cause to Lyme disease are used to immunize animals and detect immune responses
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DB; AAF29032.
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73; Conservative
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99.78;
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18-JUN-1999;

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Matches 372;
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(BROO-)
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              Chimeric -
Chimeric -
                                    Borrelia; ospC;
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                                                    Borrelia
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DB; AAF29042.
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BROOK BIOTECHNOLOGIES IN
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             Borrelia
Borrelia
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98.7%;
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                                                   protein
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Pred. No. 5.6e-118;
2; Mismatches 0;
                                     vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
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Lyme disease are used
to Lyme disease -
                                                                                                                                                                                                                                                                                                                               Sequence
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98.1%;
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d to immunize
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                  375
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                                                                                                                                                                                                                                                                            Score 1810.5; DB 22; Pred. No. 2.2e-117; 2; Mismatches 2; 1
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detect immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 43; Page 81; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dattwyler RJ,
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Chimeric - Borrelia
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                                                                                                                             KAKKCSBEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSK 360
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                                                                                                                                                             {\tt ltspvvaespamvnnsgkdgntsansadesvkgpnlteiskkitesnavvlavkeletll}
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DB; AAF29015.
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                        Protein;
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87.7%; Pred. No. 2.4e-102;
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Lyme disease are used
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Chimeric - |
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                                           KAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSK
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Pred. No. 4.2e-102;
1; Mismatches 25;
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Chimeric -
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DB; AAF29043.
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Borrelia sp.
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86.4%;
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Pred. No. 4.3e-101;
2; Mismatches 25;
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N-PSDB; AAF29017.
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85.9%; Pred. No. 1.7e-100;
tive 22; Mismatches 27;
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                                                                                                                                                                                                                                          (UYNY )
(BROO-)
                                                                                                                                              Sequence
                                                                                                                                                                                                                       Claim 43; Page 91-92;
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Chimeric - Borrelia
121 KLKEKHTDLGKEGYTDADAKEAILKTNGT-KTKGAEELGKLFESVEVLSKAAKEMLANSV
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Pred. No. 5.8e-98;
9; Mismatches 32;
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Local Si hes 326;

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                                                      The present invention provides compositions comprising ospc protein chimeric ospc proteins from members of the Borrelia genus. These mo Borrelia burgdorferi, B. afzelii or B. gazinii. These can be used vaccines against Borrelia infection, which is spread by ticks and
Sequence
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(BROO-)
                                                                                                                                                                       Claim 43; Page 128-129; 160pp;
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Query Match

81

18

Score 1493;

DB

22;

Length 368;

The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea

be

Sequence

368

Lyme

disease.

Claim 43; Page 99-100;

160pp;

English

The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzeli or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads

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Chimeric
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Lyme disease are used
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N-PSDB; AAF29028.
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                                                                                      Claim 43; Page 112-113; 160pp;
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Best Local S
Matches 313
     Compositions of OspC polypeptides Lyme disease are used to immunize to Lyme disease -
                                  WPI; 2001-050113/06.
N-PSDB; AAF29038.
                                                                                                                                                              Chimeric - 1
Chimeric - 1
                                                          Dattwyler RJ,
                                                                                                             19-JUN-2000; 2000WO-US16915
                                                                      (UYNY ) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
                                                                                                 18-JUN-1999;
                                                                                                                                28-DEC-2000
                                                                                                                                               WO200078966-A1
                                                                                                                                                                             Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick.
                                                                                                                                                                                             Borrelia sp chimeric ospC protein SEQ ID NO:
                                                                                                                                                                                                                    03-APR-2001
                                                                                                                                                                                                                                             AAB62734 standard; Protein;
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                                                                                                                                                                                                                                                                                     361 lkaaqvaltnsvkel 375
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Borrelia
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83.5%;
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Pred. No. 3.6e-95;
       from strains of Bor
animals and detect
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                                                       Luft
                                                      ВJ,
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           Borrelia which cause
                                                   Gomes-Solecki M;
    immune responses
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                                                                                                                                                                  18-JUN-1999;
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83:2%; Pred. No. 3.1e-95;
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Chimeric -
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1: /cgn2_6/ptodata/2

2: //gn2_6/ptodata/2/

3: /cgn2_6/ptodata/2/

4: /cgn2_6/ptodata/2/
5: //gn2_6/ptodata/2/
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Match
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-08-235-836C-107
US-08-158-353-2
US-08-158-353-2
US-08-158-353-4
US-08-158-353-4
US-08-158-353-4
US-08-235-836C-34
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US-08-235-836C-34
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US-08-235-836C-36
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US-08-328-254-6
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PCT-US94-10261A-24
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US-08-685-576-1
US-08-685-576-1
US-08-685-576-1
US-08-685-576-1
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US-08-685-576-1
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Sequence 112, Appli
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1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60

Query Match
Best Local Similarity
Matches 229; Conserv

Conservative

31;

Score 964; DB 4 Pred. No. 7e-62; 1; Mismatches

DB 4; 92;

Length 466; Indels 32;

9

52.3%;

PRIOK APPLICATION DATA: PRIOK APPLICATION NUMBER: US 08/148,191 FILING DATE: 01-11-93 ATTORNEY/AGENT INFORMATION: NAME: BOGSSIAN, MAGGARET C. REGISTRATION NUMBER: 25,324 REFERENCE/DOCKET NUMBER: 35,324 REFERENCE/DOCKET NUMBER: BNL93-28A TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338 TELECHONE: (516) 282-7338 TELECHATION FOR SEQ ID NO: 110: SEQUENCE CHARACTERISTICS: LENGTH: 466 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-235-836C-110	1 235-836C-110 ence 110, Application US/08235836C ence 110, 6248562 ence 110, 20nn, John J. epplicanT: Dunn, John J. epplicanT: No. 6248562el Chimeric Proteins Compris ITLE OF INVENTION: Borielia Polypeptides and Uses Therefor UMBER OF SEQUENCES: 144 ORRESPONDENCE ADDRESS: ADDRESSE: Brookhaven National Laboratory STREET: UPton STATE: NY COUNTRY: USA ELT: 11973 OMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Tabm PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 URRENT APPLICATION DATA: APPLICATION UMBER: US/08/235,836C ETLING DATE: 29-APR-1994 CLASSIFICATION: 435	28 145 7.9 1663 5 PCT-US93-07261-16 Sequence 29 145 7.9 3111 2 US-08-460-309-4 Sequence 31 143.5 7.8 630 4 US-08-973-462-9 Sequence 32 143.5 7.8 1630 4 US-08-973-462-9 Sequence 34 141 7.7 1786 4 US-08-973-462-8 Sequence 35 139 7.5 1285 4 US-09-184-18 Sequence 36 138.5 7.5 1098 4 US-09-28-928-8 Sequence 37 138.5 7.5 1104 4 US-08-923-9928-8 Sequence 38 137 7.4 1104 4 US-08-923-9928-4 Sequence 41 133.5 7.4 1388 2 US-08-923-9928-4 Sequence 41 133.5 7.2 641 4 US-08-923-9928-4 Sequence 42 132.5 7.2 1561 3 US-08-931-160 Sequence 43 131.5 7.1 1068 4 US-08-931-938-11 Sequence 44 133.5 7.2 1561 3 US-08-931-938-11 Sequence 131 7.1 1068 4 US-08-931-938-11 Sequence 131 7.1 1068 4 US-08-931-938-11 Sequence 131 7.1 1093 5 PCT-US93-03077-1 Sequence Sequence 130.5 7.1 396 1 US-08-430-024-2 Sequence Sequence 130.5 7.1 396 1 US-08-430-024-2 Sequence Sequence 130.5 7.1 396 1 US-08-430-024-2 Sequence 130.5 7.1 396 1 US-08-430-024-2
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RESULT 2
US-08-235-836C-30
; Sequence 30, App
: ---- 62485
                                                    US-08-235-836C-30
                                                                                                                               TELEFAX: (516) 282-372
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                  NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
                                                              TOPOLOGY: lin
                                                                                        LENGTH: 210 amino
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 29-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 AEKTTLVVKEGTVTLSKNISKSGE 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 S-KDKSSTEEKFNEKGEVSEKITTRADG--TRLEYTGIKSDGSGKAKEVLKGYVLEGTLT 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 LELKGTSDKNNGSGVLEGVKADKSKVKLTIS-----DDLGQTTLEVFKEDGKTLVSKKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 VETLLTS-----IDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLI--SNLITKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 ELTSPVVAESPKKPKQNVSSLD---EKNSVSVDLPGEMKVLVSKEKNKDGKYDLIATVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEKLFESV-----KNLSKAAK 363
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                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorfer1
FILE REFERENCE: 738.0010S2
CCURRENT APPLICATION NUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER FILING DATE: 1994-03-10
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1990-12-21
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER FILING DATE: 1989-12-22
EARLIER FILING DATE: 1990-06-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 209
TYPE: PRT
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Best Local Similarity
Matches 188; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fuchs, Renate APPLICANT: Motz, Manfred APPLICANT: Soutscheck, E.
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Best Local Similarity
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181 ELTSPVVAESP
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                                       KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                           KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                           IGKKTHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN
                                                                                                                            IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETETN 120
                                                                                                                                                                            ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA
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98.4%;
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Pred. No. 9.5e-60;
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Pred. No. 4.9e-60;
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                                                                               RESULT 5
US-08-235-836C-122
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US-08-158-353-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: CARIFOLL, ALICE O.
REGISTRATION NUMBER: 33,542
REFERENCE, DOCKET NUMBER: UCT9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPHONE: 617-861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                Sequence 122, Application US/08235836C Patent No. 6248562 GENERAL INFORMATION:
APPLICANT: Dunn, John J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08158353 Patent No. 5620862
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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TITLE OF INVENTION: Methods for
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, S.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Mili
CITY: Lexington
STATE: MA
                                                                                                                                                                             181 ELTSPVVAESP 191
                                                                                                                                                                                                            137
                                                                                                                                                                                                                                          121
                                                                                                                                                197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
                                                                                                                                                                                                                                                                     KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                                                                                                                                    ELTSPVVAESP 207
                                                                                                                                                                                                            KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 amino acids
Dunn, John J.
Luft, Benjamin J.
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Methods for Diagnosing Early Lyme
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 928; DB 1; Length 210; Pred. No. 9.5e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                 Sequence 15, Application US/08209603E Patent No. 6248538
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TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/235
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MATGAIEt C.
REGISTRATION NUMBER: 25,324
BEFERENKE CONCETT NUMBER: 231
                                                                                                                                                                   GENERAL INFORMATION:
                                                                   APPLICANT: FUCHS, RENATE
APPLICANT: WILSKE, BETTINA
APPLICANT: PREAC-WURSIC, VERA
APPLICANT: MOTZ, MANFRED
APPLICANT: SOUTSCHECK, ERWIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NO TITLE OF INVENTION: BO NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
               TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS TITLE OF INVENTION: FROM BORRELIA BURGDORFERI NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: BN TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                    466 SPVVAESPKKPGTMAQYNQMHMLSNKSASQNVRTAEE 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Brookhaven National Laboratory
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11973
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Pred. No. 4.3e-59;
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RESULT 7
US-08-23-836C-107
: Sequence 107, Application US/08235836C
: Patent No. 6248562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 436
PRIOR APPLICATION INDEER: PCT/EP90/02282
APPLICATION NUMBER: PCT/EP90/02282
FILING DATE: 21-DEC-1990
FILING DATE: 19-UN-1992
ATTORNEY/ACENT INFORMATION:
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9217-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEPAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                          197 ELTSPVVAESP 207
                                                                                                                     181 ELTSPVVAESP 191
                                                                                                                                              121 KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGABELGKLFESVEVLSKAAKEMLANSVK 180
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ORIGINAL SOURCE:
                                                                                                                                                                                                    61 IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
DESCRIPTION: PROTEIN
                                                                                                                                                                                                                                          17 ISCNNSGKOGNTSANSADESVKGPNLTEISKKITDSNAVLLAVLEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                          1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
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CURRENT APPLICATION UMBER: US/08/209,603E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: ATAT - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
TOPOLOGY: LINEAR
                                                                                                                                 KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                                                                                                                                                      IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
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STREET: 99 PARK
CITY: NEW YORK
STATE: NY
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9 PARK AVENUE
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                                                                                                                                                                                                                                                                                                          Mismatches
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GENERAL INFORMATION:
APPLICANT: Padula, Steve
TITLE OF INVENTION MELT
TITLE OF INVENTION Disc
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                              Sequence 2, Application US/08158353
Patent No. 5620862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-235-836C-107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           456 SPVVAESP 463
                                                                                                                                                                                                                                        184 SPVVAESP 191
                                                                                                                                                                                                                                                                    124 EKHTDLGKEGYTDADAKEATLKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT 183
              ADDRESSEE:
                                                                                                                                                                                                                                                      396 AKHTDIGKEGYTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT 455
                                                                                                                                                                                                                                                                                                                 336 KIHQNNGLDTEYNHNGSLLAGRYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTNKLK
                                                                                                                                                                                                                                                                                                                                                                         NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNI
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                64 KIHONNGLDTEYNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTNKLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 01 FILING DATE: 01-11-93 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/01
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 98.98;
es 186; Conservation
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TYPE: a
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APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrella Polypeptides and Uses Therefor
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CITY: Upton
STATE: NY
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    Hamilton, Brook,
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                                                    Steven J.

Methods for Diagnosing Early Lyme
Disease
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Pred. No. 2.3e-58;
0; Mismatches 2
Smith & Reynolds, P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Applic Patent No. 5530103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
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TELEFAX: 617-861-9540
TELEF
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LIVEY, Ian
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND
TITLE OF INVENTION: PREVENTION
                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSE: FOLEY & Lardner
STREET: 3000 K Street, N.W.,
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 DKLKSSHAELGIANGAATDANAKAAILKTNGTKDKGAQELEKLFESVKNLSKAAQETLNN 195
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CITY: L
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 SVKELTSPVVAENP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 NKLKEKHTDLG--KEGYTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLAN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETFT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
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                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 145; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02173
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Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                METHOD AND COMPOSITION FOR PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.7%; Score 676; DB 1; L
74.7%; Pred. No. 1.2e-41;
tive 18; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/158,353
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                                                                                                                                                                                                                                                                                        Suite 500
Version #1.25
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US-07-903-580-2
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Patent No. 6221363
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                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202,672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/903,580 FILING DATE: 25-JUN-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/824,161 FILING DATE: 22-JAN-1992
                                                                                                                                                                                         APPLICANT: LIVEY, Ian
APPLICANT: DORNER, FEIGHICH
TITLE OF INVENTION: METHOD AND COMPOSITION FOR THE
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,245
FILING DATE: 11-JUL-1991
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      179 VKELTSPVVAESP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS 196
                                                                                                                STREET: 1800 Dia
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                   ZIP:
                                                                                                 COUNTRY:
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                                                                                                                                                                 ADDRESSEE:
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                                                                                   22313-0299
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                                                                                                 Virginia
Y: USA
                                                                                                                                                                                                                                                                                                                   Application US/07903580
                                                                                                                                                E: Foley & Lardner
1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 amino acids
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PatentIn Release #1.0,
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73.6%;
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Pred. No. 1.5e-40;
                                                                                                                                                 Suite 500
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Version #1.25
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Patent No. 5620862
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 142; Conserv
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                                                                                                                                                                                                                                                                                                                                                                               08-158-353-4
                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                          APPLICANT: Padula,
                                                                                                                                                                                                                                                                                                                                                                                                                                       179 VKELTSPVVAESP 191
|||||||||||
197 VKELTSPVVAETP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (702)836-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 TNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/824,161
FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,245
FILING DATE: 11-JUL-1991
CLASSIFICATION: 435
                          APPLICATION NUMBER: US/08/158,353
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NAME: BENT, Stephen A.
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEG-LKEKIDAAKKCSETF 118
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                                                                                                                                                   02173
                                                                                                                                                                                             Lexington
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Methods for Diagnosing Early Lyme
Disease
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73.6%;
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Pred. No. 1.5e-40;
14; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30472/131
                                                                                                                                                                                                                        Smith & Reynolds, P.C.
                                                         Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 212;
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; ORGANISM: Borrelia
US-09-196-293-11
                                                                                                                                                                    APPLICANT: MOLZ, Manfred

APPLICANT: Milske, Bettina

APPLICANT: Wilske, Bettina

APPLICANT: Wilske, Bettina

APPLICANT: Preac-Mursic, Vera

TITLE OF INVENTION: Active proteins from Borrelia

FILE REFERENCE: 738.001052

CURRENT APPLICATION NUMBER: U5/09/196.293

CURRENT FILING DATE: 1998-11-19

EARLIER APPLICATION NUMBER: US 07/862,535

EARLIER APPLICATION NUMBER: US 07/862,535

EARLIER APPLICATION NUMBER: US 07/862,535

EARLIER APPLICATION NUMBER: WO PCT/EP90/02282

EARLIER FILING DATE: 1990-12-21

EARLIER APPLICATION NUMBER: DE 939 42 728.5

EARLIER APPLICATION NUMBER: DE 939 42 728.5

EARLIER APPLICATION NUMBER: DE 939 42 728.5
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                                                          SEQ ID NO 11
LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: US-08-158-353-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11,
                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                             EARLIER APPLICATION NUMBER: DE P40 18 988.0 EARLIER FILING DATE: 1990-06-13 NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fuchs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 VKELTSPVVAESP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 VKELTSPVVAESP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 TNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 AIGKKIHONNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKK 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MACNNSGKDGNT-SANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAK 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1, Application US/09196293
6183755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS: single
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.3%; Score 614; DB 1; 69.9%; Pred. No. 3.5e-37; tive 14; Mismatches 42
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Pred. No. 4.8e-37;

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Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-335
TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 11:
                 HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8-209-603E-11
                                                                                                    TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                           FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRAFION NUMBER: 27,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTITE OF INVENTION: FROM BORRELIA BURGDORFERI NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: PCT/EP90/02282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 VKELTSPVVAESP 191
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197 VKELTSPVVAESP 209
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                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/EP90/0228: FILING DATE: 21-DEC-1990 APPLICATION NUMBER: US 07/862,535
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/209,603E FILING DATE: 10-MAR-1994 CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
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                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9217-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                        DESCRIPTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
ORGANISM: B. BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MACNNSGKDG-NTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAK 59
                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08209603E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUCHS, RENATE WILSKE, BETTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOUTSCHECK, ERWIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WILSKE, BETTINA PREAC-MURSIC, VERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOTZ, MANFRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BROOKS HAIDT HAFFNER & DELAHUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MS-DOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMUNOLOGICALLY ACTIVE PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34,
                            TELEFAX: (516) 282-372
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                         NAME: Bogosian, Margaret C.
REGISTATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                               APPLICATION NUMBER: US 0:
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 29-API
                                                                                        TELEPHONE:
                   ENGTH:
amino acid
                 212 amino acids
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516)

282-7338

282-3729

29-APR-1994

US/08/235,836C

US 08/148,191

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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-209-603E-11
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-235-836C-34
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Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                       APPLICANT: Dunn, John J.

APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins
TITLE OF INVENTION: Borrelia Polypeptides and Uses T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
ANTI-SENSE: N/A
                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOME:
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                                                                                                                                                                                CITY: Upton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY:
                                                                                                                                                                                                                      ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                  6248562
                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08235836C
                                                                                                                                         USA
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70.5%;
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.N/A
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2.

; TOPOLOGY: linear; MOLECULE TYPE: prof US-08-235-836C-34

protein

Length 212;

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-235-836C-32
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US-08-235-836C-32
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                Query Match
Best Local Similarity
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                                                                                                                                                                       TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: I
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MATGRATET C.
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
CITY: Upton
CITY: NY
US
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 VKELTSPVVAESP 191
||||||||||
197 VKELTSPVVAESP 209
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                                                                                                                                                                                                                                                                                                               NAME: Bogosian, Margaret C
REGISTRATION NUMBER: 25,32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 TNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 AIGGKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                       (516) 282-7338
                    32.6%;
68.2%;
              Score 600.5; DB 4;
Pred. No. 3.2e-36;
                                 Length 209;
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            180 KELTSPVVAESP 191
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                                                                                                                                    KELTNPVVAESP 206
                                    NRLKGSHAQLGVAAATDDHAKEAILKSNPTKDKGAKALKDLSESVESLAKAAQEALANSV 194
                                                 NKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSV 179
                                                                              IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETFT 119
                                                                                                                      ISCNNSG--GDTASTNPDESAKGPNLTVISKKITDSNAFVLAVKEVEALISSIDELANKA 74
                                                                                                                                                                  19;
                                                                                                                                                                  Mismatches
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Search completed: March 18, Job time: 345 sec 2002, 09:55:32

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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BCD
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1842
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/cgn2_6/ptodata/2/paa/US086_COMB.pep:*
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SUMMARIES
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4684596	Result
1842 1837 1834 1834 1819.5 1819.5 1810.5 1810.5 1897.5	Score
100.0 99.7 99.6 99.8 98.8 98.8 98.3 98.3	Query Match
	Length DB
19 19 19 19 19 19	!
US-09-596-746A-24 US-09-596-746-24 US-09-596-746-60 US-09-596-746A-60 US-09-596-746A-80 US-09-596-746A-80 US-09-596-746A-80 US-09-596-746A-28 US-09-596-746A-28	ID
Sequence 24, Sequence 24, Sequence 60, Sequence 60, Sequence 80, Sequence 80, Sequence 28, Sequence 28, Sequence 28, Sequence 28,	Description
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205.	1209.5	209.	212.	213.	213.	217.	245.	245.	48.	253.	281.	81.	284.	289.	48	48	48	49	49	49	49	49	49	49	52	52	52	53	56	56	57	57	589.	1589.5	592.
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-09-596-746-7	9-596-7	-09-596-746-68	-09-596-746-3	-09-596-746A-	-09-596-746-5	-09-596-746A-3	9-596-746A-	-09-596-746-7	-09-596-746-4	09-596-746A-4	-09-596-7462	-09-596-746-	-09-596-746-	-09-596-746A-3	-09-596-746A	-09-596-7	-09-596-746-	-09-596-7462	-09-596-746-	-09-596-7462	-09-596-746-	-09-596-746A	9-596-746-40	-09-596-746A-	-09-596-746A-6	-09-596-746-6	-09-596-746-3	-09-596-746A-	-09-596-746A-3	-09-596-746-3	S-09-596-746A-	S-09-596-746-8	-09-596-746A-	S-09-59	-09-596-746-2
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ALIGNMENTS

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; FEATURE: ; OTHER INFORMATION: OSPC Chimera US-09-596-746A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-596-746A-24; Sequence 24, Application US/09596746A; GENERAL INFORMATION:
                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 375
Query Match
Best Local Similarity
Matches 375; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/596,746A CURRENT FILING DATE: 2000-06-19 PRIOR APPLICATION NUMBER: US 60/140,042 PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D:
FILE REFERENCE: 2631.1002-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                   LENGTH: 375
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dattwyler, Raymond J.
Seinost, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dykhuizen, Danial
                  100.0%;
  Score 1842; DB 19;
Pred. No. 8.8e-125;
Mismatches 0;
                                     Length 375;
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Conservative

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GENERAL IMPORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Dattwyler, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: Groups of Borrelia burgdorferi and FITLE OF INVENTION: Groups of Borrelia burgdorferi and FITLE REFERENCE: 2631,1002-001.
CURRENT APPLICATION NUMBER: US/09/596,746
PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: OSPC Chimera US-09-596-746-24
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.7
Best Local Similarity 100.
Matches 374; Conservative
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182 LTSPVVAESPAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                       122 LKEKHTDLGKEGYTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE 181
                                                                                                                                                                                                        62 GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETNK 121
                                                                                                                                                                                  61 GKKIHONNGLDTEYNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTNK
                                                                                                                                                                                                                                                                                                                2 ACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI 61
                                                                              LKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE
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                                                                                                                                                                                                                                                                                    ACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 LTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 LTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIE 300
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                                                                                                                                                                                                                                                                                                                                                                                                99.7%; Score 1837; DB 19
100.0%; Pred. No. 2e-124;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19; Length 374;
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APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Dykhnizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J. C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
FILE OF INVENTION: Borrelia affectii That Cause Lyme Disea
FILE REFERENCE: 2631.1002.001
CURRENT APPLICATION NUMBER: US/09/596,746
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: B9-06-18
SOFTWARE: PRAFERO for William Willia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: ospC Chimera
US-09-596-746-60
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LENGTH: 398
TYPE: PRT
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Best Local Similarity
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                                                       362 AKEMLTNSVKELTS
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                                                                                                                                                                                                                      TSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEK 301
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                         398
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Cause Lyme Disease in

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324

264 241 144

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APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzeili That Cause Lyme Diser
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION UNMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
; APPLICANT: Luft, Benjamin J.;
; APPLICANT: Maria J.C. Gomes-Solecki
; TITLE OF INVENTION: Groups of Borrelia burgdorferi and
; TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
; FILE REFERENCE: 2631.1002-001
; CURRENT APPLICATION NUMBER: US/09/596,746
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/140,042
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; Sequence 60, Application US/09596746A; GENERAL INFORMATION:
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US-09-596-746-80
Sequence 80, Application US/09596746
GENERAL INFORMATION:
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SEQ ID NO 60
LENGTH: 399
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APPLICANT:
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Matches
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ORGANISM: ospC Chimera
09-596-746A-60
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les 373; Conserv
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Dykhuizen, Danial
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Dykhuizen, Danial
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; LENGTH: 401
; TYPE: PRT
; ORGANISM: OSPC Chimera
US-09-596-746-80
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                                                                ; LENGTH: 402
; TYPE: PRT
; ORGANISM: ospC Chimera
US-09-596-746A-80
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: Sequence 80, Application US/09596746A

: GEMERAL INFORMATION:
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Best Local Simi
Matches 372;
                                                                                                                   SOFTWARE: 1
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Query Match
Best Local Similarity
Matches 372; Conserv
                                                                                                                                     APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US.09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US.60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                            APPLICANT: Dattwyler, Raymond J. APPLICANT: Seinost, Gerald APPLICANT: Dykhuizen, Danial
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NUMBER OF SEQ ID NOS:
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          98.8%;
98.7%;
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Score 1819.5; DB 19;
Pred. No. 4.1e-123;
2; Mismatches 0; I
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; OTHER INFORMATION: OSPC Chimera US-09-596-746-28
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GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-
NUMBER OF SEQ ID NOS: 84
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 ELTSPVVAES---PAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEV
                                   KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                              IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
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Maria J.C. Gomes-
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milarity 98.1%;
Conservative
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LSKAAKEMLTNSVKELTS
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APPLICANT: Dykhulzen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: OSPC Chimera US-09-596-746A-28
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ORGANISM: Artificial Sequence
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nes 371; Conserv
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LSKAAKEMLTNSVKELTS 375
                                                              EIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKN
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98.1%;
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Pred. No. 1.7e-122;
2; Mismatches 2; ]
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US-09-596-746A-26

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TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Dise.
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FASTSEQ for Windows Version 4.0
TYPE: PRT
TYPE: PRT
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Sequence 26, Application US/09596746
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Sykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
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Best Local Similarity
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APPLICANT: Maria J.C. Gomes-Solecki
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87.7%; Pred. No. 4.3e-107;
tive 20; Mismatches 25;
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
TENCTORY
                            APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdc
TITLE OF INVENTION: Borrelia afzelii That Cau
FILE REFERENCE: 2631,1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
LENGTH: 397
TYPE: PRT
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; TYPE: PRT
; ORGANISM: OSPC Chimera
US-09-596-746-62
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                                                                                                                                                                                                                                                                                                                                             Sequence 62,
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TYPE: PRT
ORGANISM: Artificial Sequence
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87.7%;
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                                                                                                                                                                                                        Cause
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Query Match Best Local :

Similarity

86.3%;

Score 1589.5; DB 1 Pred. No. 1.8e-106;

DB 19;

Length

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; ORGANISM: OSPC
US-09-596-746A-62
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                                                                                                                                                                                                                                                   SEQ ID NO 62
LENGTH: 398
                                                                                                                                             Matches 326;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Groups of Borrelia burgdorferi
TITLE OF INVENTION: Borrelia afzelii That Cause Lyn
FILE REFERENCE: 2631.1002-001
                                                                                                                                                                                                                                                                              SOFTWARE:
              122
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                                                    GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK 121
                                                                                                        ACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI 61
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                                                                                          SCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI 85
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Luft, Benjamin J.
Maria J.C. Gomes-Solecki
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Pred. No. 1.8e-106;
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US-09-596-746-82
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SEQ ID NO 82
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APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi an
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
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TYPE: PRT
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                                                                                                                                                                          LTSPVVAES---PAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVE 238
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   LSKAAKEMLTNSVKEL
                                                                                               TLLASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKE 324
                                                                                                                         TLLTSIDELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA 297
                                                                                                                                                                                                                                       LKEKHTDLGKEGUTDADAKEAILKINGTKIKGAEELGKLFESVEVLSKAAKEMLANSVKE 181
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Seinost, Gerald
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86.4%;
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Pred. No. 2e-105;
22; Mismatches 25;
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25;
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RESULT 15
US-09-596-746-30
US-09-596-746-30
; Sequence 30, Application US/09596746
; GENERAL INFORMATION:
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: Sequence 82, Application US/09596746A
: GENERAL INFORMATION:
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Best Local Similarity
Matches 325; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Groups of Borrella burgdorferi and TITLE OF INVENTION: Borrella afzelli That Cause Lyme Disease in Humans FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 401
TYPE: PRT
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhulzen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
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APPLICANT: Maria J.C. Gomes-Solecki
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86.4%; Pred. No. 2e-105;
vative 22; Mismatches 25; Indels 4
      Disease
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
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               NLSKAAKEMLTNSVKEL 373
                                                       EKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVE
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Pred. No. 8.3e-105;
2; Mismatches 27;
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Search completed: March 18, 2002, 10:08:42 Job time: 970 sec

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Result
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Perfect score:
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Maximum
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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Copyright (c) 1993 - 2000 Comp
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US-10-032-885-7646

US-10-072-851-15045

US-09-708-427-15045

US-09-748-875-61

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US-09-748-875-60

US-09-815-242-5883

US-09-815-242-13080

US-09-748-875-60

US-09-748-875-60

US-09-748-875-60

US-09-748-875-60

US-09-748-875-60

US-09-748-875-60

US-09-748-875-60

US-09-38-275-7

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Sequence 5, Appli
Sequence 3, Appli
Sequence 19883, A
Sequence 19882, A
Sequence 19881, A
Sequence 15044, A
Sequence 15590, A
Sequence 1545, A
Sequence 14, Appli
Sequence 61, Appli
Sequence 62, Appli
Sequence 62, Appli
Sequence 5883, Ap
Sequence 5883, Ap
Sequence 13080, A
Sequence 13080, A
Sequence 13080, A
Sequence 13080, A
Sequence 12, Appli
Sequence 17, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 13080, A
Sequence 15046, A
Sequence 15046, A
Sequence 15046, A
Sequence 15046, A
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Sequence 5639, Ap		Sequence 9, Appli	Sequence 113, App	Sequence 6, Appli		Sequence 3, Appli		Sequence 3730, Ap	Sequence 10311, A	Sequence 10224, A	Sequence 63, Appl	Sequence 5834, Ap	Sequence 5834, Ap	Sequence 21159, A	Sequence 21160, A	Sequence 21161, A	Sequence 12996, A	Sequence 12996, A	Sequence 5835, Ap

ALIGNMENTS

US-09-974-992-5

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CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 211
RESULT 2
US-09-974-992-7
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US-09-974-992-5
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GENERAL INFORMATION:
APPLICANT: Mathiesen, Marianne J.
APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 148; Conserv
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                                                        179 VKELTSPVVAESP 191
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196 VKELTSPVVVESP 208
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                                                                                                                                                                                                61 IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLK-NEGLKEKIDAAKKCSETFT 119
                                                                                                                                                                                                                                            17 ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEL-AKA
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                                                                                                                                                                                                                                                                                                                     36.6%;
                                                                                                                                                                                                                                                                                                       11;
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Pred. No. 2.4e-39;
1; Mismatches 31;
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CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 212
TYPE: PRT
ORGANISM: Borrelia afzelii
US-09-974-992-7
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US-09-974-992-3
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     Query Match 31.9%;
Best Local Similarity 66.5%;
Matches 127; Conservative 2
                                                                                                                                       SOFTWARE: PatentIn Ver.
SEQ ID NO 3
LENGTH: 207
TYPE: PRT
                                                                                                   ORGANISM: Borrelia garinii
-09-974-992-3
                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                              APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.3%; Score 614; DB 6; Best Local Similarity 69.9%; Pred. No. 3.4e-35; Matches 135; Conservative 14; Mismatches 42
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NETAL INFORMATION:

APPLICANT: Mathiesen, Marianne J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide
FILE REFERENCE: 459-666P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mathiesen, Marianne J. APPLICANT: Theisen, Michael
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197 VKELTSPVVAESP 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF
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         24;
   Score 587.5; DB 6;
Pred. No. 2.2e-33;
24; Mismatches 37;
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ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
COATION: 1..1014
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..1014
COTHER INFORMATION: Ceres Seq. ID 1836847
US-09-708-427-19883
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US-09-708-427-19883
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SQ ID NO 1983
LENGTH. 1014
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 118; Conserv
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
695
                                                                                                 236
                                                                                                                                                                                              575 RDLEGKIKSYEEQLAEASGKSSSLKEKLEQTLGRLAAAESVNEKLKQEFDQAQEKSLQSS 634
                                                                                                                                                                                                                                127 TDL-GKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSP 185
                                                                                                                                                                                                                                                                    517 AEESLEQKG--REIDEATTKRMELEALHQSLSIDSEHRLQKAMEEFTSRDSEASSLTEKL 574
                                                                                                                                                                                                                                                                                                                                         461 LEA---TVDEYSVKISESENLLESIRNELNVTQG-KLESIENDLKAAGLQESEVMEKLKS
                                                                                                                                                                                                                                                                                                                                                                                                               401 KHGETEADSKGYLGQVAELQSTLEAFQVKSSSLEAALNIATENEKELTENLNAVTSEKKK 460
                                                                                                                                                                                                                                                                                                       95 KLDGLKNEGLKEKIDAA-----LKEKH 126
                                                                                                                                                                                                                                                                                                                                                                           46 VEALLSSIDEIAAK------AIGKKIHQNNGLDTEYNHNGSLLAGAYAISTL--IKQ 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 KLKDSHAELGIQSVQDDNAKKAILKTHGTKDKGAKELEELFKSLESLSKAAQAALTNSVK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ELTSPVVAESP 191
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                                                                                                                         SESELLAETNNQLKIKIQELEGLIGSGSVEKETALKRLEEAIERFNQKETESSDLVEKLK 694
                                                                                                                                                          VVAESPAMVNNSGK-----DGNTSANSADESVKGPNLTE----ISKKITESNAVVLAVK 235
                                                     THENQIEEYKKLAHEASGVADTRKVELEDALSKLKNLESTIEELGAKCQGLEKESGDLAE 754
                                                                                             EVETLLTSIDELA-KAIG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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: NAME/KEY: misc_feature
: LOCATION: 1..1018
: OTHER INFORMATION: Xaa is a
: NAME/KEY: misc_feature
: LOCATION: 1..1018
: OTHER INFORMATION: Ceres Se
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US-09-708-427-19882
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION ON 1005: 85364
SOPTWARE: Patentin version 3.1
SEQ ID NOS: 84364
SOPTWARE: Patentin version 3.1
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Best Local Similarity
Matches 118; Conserv
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                    812
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                                                                                                                                                                                                                                                                                                                                                                                                             95 KLDGLKNEGLKEKIDAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 VEALLSSIDEIAAK-----AIGKKIHQNNGLDTEYNHNGSLLAGAYAISTL--IKO 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 KDGNTSANSADE-----SVKGPNL----TEISKKITDS-NAVLLAVKE 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVK-NLSKAAKEMLTNSVK- 371
                                                KGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVK-NLSKAAKEMLTNSVK- 371
                                                                                                                                                            THENQIEEYKKLAHEASGVADTRKVELEDALSKLKNLESTIEELGAKCQGLEKESGDLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AELTS 866
                                                                                                                                                                                              EVETLLTSIDELA-KAIG------KKIKN----
                                                                                                                                                                                                                               SESELLAETHNQLKIKIQELEGLIGSGSVEKETALKRLEEAIERFNQKETESSDLVEKLK
                                                                                                                                                                                                                                                                                                     RDLEGKIKSYEEQLAEASGKSSSLKEKLEQTLGRLAAAESVNEKLKQEFDQAQEKSLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LEA---TVDEYSVKISESENLLESIRNELNVTQG-KLESIENDLKAAGLQESEVMEKLKS 520
                                                                                                                      -DVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA-EIEKAKKCSEEFTAKL--
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                    EGEKLQSQIEKLRAVAAEKSVLESH----
                                                                                      VNLKLNLELANHGS-----EANELQTKLSALEAEKEQTANELEASKTTIEDLTKQLTS
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Pred. No. 0.0004;
0; Mismatches 161; Indels 136;
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                    -- FEELEKTLSEVKAQLKENVENAATASVKV
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RESULT
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CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 19881
LENGTH: 1269
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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                                                       AELTS 1121
                                                                                                                         EGEKLQSQIEKLRAVAAEKSVLESH-----FEELEKTLSEVKAQLKENVENAATASVKV 1116
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RESULT 6
US-09-708-427-19881
; Sequence 19881, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; TITLE OF INVENTION: THEREBY
                                                                                                                                                       950 THENQIEEYKKLAHEASGVADTRKVELEDALSKLKNLESTIEELGAKCQGLEKESGDLAE 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    772 AEESLEQKG--REIDEATTKRMELEALHQSLSIDSEHRLQKAMEEFTSRDSEASSLTEKL 829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 VEALLSSIDEIAAK------AIGKKIHQNNGLDTEYNHNGSLLAGAYAISTL--IKQ 94
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VNLKLNLELANHGS-----EANELQTKLSALEAEKEQTANELEASKTTIEDLTKQLTS 1062
                                            -DVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA-EIEKAKKCSEEFTAKL-- 313
                                                                                                                                                                                                                                                                                                                  SESELLAETNNQLKIKIQELEGLIGSGSVEKETALKRLEEAIERFNQKETESSDLVEKLK 949
                                                                                                                                                                                                                                                                                                                                                                                           VVAESPAMVNNSGK-----DGNTSANSADESVKGPNLTE----ISKKITESNAVVLAVK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDLEGKIKSYEEQLAEASGKSSSLKEKLEQTLGRLAAAESVNEKLKQEFDQAQEKSLQSS 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDL-GKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSP 185
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US-09-708-427-15044

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RESULT 8
US-10-032-585-7646
Sequence 7646, Application US/10032585
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
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; NAME/KEY: misc_feature
LOCATION: 1..1313
OTHER INFORMATION: Xaa is any amino acid
; LOCATION: 1..1313
; OTHER INFORMATION: Ceres Seq. ID 1828627
US-09-708-427-15044
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Best Local Similarity 22.2
Matches 118; Conservative
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-12439
CURRENT APPLICATION NUMBER: US/09/708,427
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATELING DATE: 2000-11-09
SOFTWARE: PATELING TO NOS: 85364
SEQ ID NO 15044
LENGTH: 1313
TYPE: PRT
                                                                                                                                                                                     439 SEAKATLLVCQEELKNC---ESQVDSLKLASKETNEKYEKMLEDARNEIDS
                                                                                                                                                                                                                 329 NAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKE----MLTNSVKELTS 375
                                                                                                                                                                                                                                                 394 SN------IQNLLDQRTELSIELERCKVEEEKSKKDMESLTLAL-------QEASTES
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                                                                                                                                                                                                                                                                          269 GSLISGAYLISNLITKKISAIKDSGELKABIEKAKKCSEEFTAKLKGEHTDLGKEGVTDD 328
                                                                                                                                                                                                                                                                                                                   334 ELLEKTIEAQRTDLEEYGRQVCIAKEÉASKLENLVESIKSELEISQEEKTRALDNEKAAT 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 VEVLSKAAKE------MLANSVKE-----LTSPVVAESPAMVNNSG-- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 QRVKHELSMTÄDAKNKALSHAEEATKIAEIHAEKAEILASELGRUKALLGSKEEKEAIEG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 ----KEGVTDADAKEAILKTNGTKTKGAE------ELGKL-----FES 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTGLMETPRSKPSPPPPRLSKLSASKSDSNSASPKVHSRLVKGTELQTQLNQIQEDLKKA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.2%; Score 169.5; DB 6; Length 1313; 22.2%; Pred. No. 0.0013; vative 60; Mismatches 140; Indels 213;
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GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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             APPLICANT:
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APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
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                                                APPLICANT:
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Best Local Similarity 20.7
Matches 98; Conservative
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TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
LENGTH: 1841
TYPE: PRT
                                                                                                                                                                                                                                                                                                                              1805 ELETEKTOTSKFKNLEERKDKEIVKLNKELELLKNDNSGAKKELSEKVSKLES 1857
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WAME/KEY: MISC_FEATURE
LOCATION: (1881)..(1881)
OTHER INFORMATION: X-any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA
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Yan...
Roemer, ...
Jiang, Bo
Tone, Charles
Howard
                                                  Trawick, John D. Yamamoto, Robert Roemer, Terry
                                                                                                                  Haselbeck, Robert
Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                        Wall, Daniel
                                                                                                                                                                                                                                                           Application US/10072851
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; LOCATION: (1881)..(1881)
; OTHER INFORMATION: X-any amino acid
US-10-072-851-15590
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                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-708-427-15045
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                                                                  CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 15045
                                                                                                                                                                                                                                                                                                     Sequence 15045, Application US/09708427 GENERAL INFORMATION:
                                                                                                                                                                                              APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: THEREBY
EILE REFERENCE: 2750-1243P
ORGANISM: Arabidopsis thaliana
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                                                  ENGTH: 1304
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Local Similarity 20.7%; Pred. No. 0.0023;
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; LOCATION: 1..1304
; OTHER INFORMATION: Ceres
US-09-708-427-15045
; ORGANISM: Streptococcus pneumoniae US-09-748-875-14
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US-09-748-875-14
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                                               TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/748,875
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR FILING DATE: 1999-04-23
RUMBER OF SEQ ID NOS: 78
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 14
LENGTH: 589
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Best Local Similarity 22.3
Matches 115; Conservative
                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09748875 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           APPLICANT: BRILES et al.
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NAME/KEY: misc_feature
LOCATION: 1..1304
OTHER INFORMATION: Xaa
                                       TYPE: PRT
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; Pred. No. 0.0015;
59; Mismatches 128;
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; Sequence 61, Application US/09748875
; GENERAL INFORMATION:
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RIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 61
LENGTH: 690
TYPE: PRT
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Best Local Similarity
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CURRENT FILING DATE: 2000-12-26
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                           QKKVEEAKKKAEDQKEKDRRNYPTITYKTLELEIAESDVEVKKAELELVKVKAKESQDEE 208
                                                                                                                                                                                  LDTE-----YNHNGSLLAGAYAIS-----TLIKQKLDGLKNEGLKEKIDA 110
                                                                              AKKCSETFTNKLKEKHTD------LGKE-GVTDADAKEAILKTNGTKTKGAEELG 158
                                                                                                                                                                                                                                                    EGVRSGNNLTVTSSGQDISKKYAD
                                                                                                                                  LITKLSEIKKKYLYDLKVNVLSEAELTSKTKETKEKLTATFEQFKKDTLPTEPEKKVAEA
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                                                                                                                                                                                                                                                                                                                                                Score 158; DB 5; 1
Pred. No. 0.0035;
9; Mismatches 149;
                                                                                                                                                                                                                                      88 SANGLHAKANTKKANTERESHIFESTIFESTER SANGER 
                                                                                                                                                                                                                                                                                                                                                                                                   Length 690;
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; TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-748-875-1
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GENERAL INFORMATION:
APPLICANT: BRILES et al.
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/748,875
CCURRENT FILING DATE: 2000-12-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 691
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PRIOR FILING DATE: 1999-04-23
                                  304 KCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAK 363
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SKKEELTSKTKAELT-----AAFEQFKKDTLKPE----KKVAEAEKKVEEAKKKAKDQK 409
                                                                                                                      IDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESVK-GPNLT-----EISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIH-QNNG
                                                                               -----KKMLSEIQLDRR-KHTQNV-----NL-NIKLSAIKTKYLYELSVLKEN
                                                                                                                                                                 VSGELATPDKKENDAKSSDSSV--GEETLPSPSLNMANESQTEHR-----KDVDEYI--
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Pred. No. 0.0035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149; Indels 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 691;
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US-09-748-875-62

Sequence 62, Application US/09748875

GENERAL INFORMATION:

APPLICANT: BRILES et al.

APPLICANT: BRILES et al.

TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR FILE REFERNCE: 454312-3140

CURRENT APPLICATION NUMBER: US/09/748,875

CURRENT FILING DATE: 2000-12-26

PRIOR APPLICATION NUMBER: 09/298,523

PRIOR APPLICATION NUMBER: 09/298,523

PRIOR FILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PATO OSCIPLIANCE OF SECULOR SEC
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Sequence 2, Application US/09748875
GENERAL INFORMATION:
APPLICART: BRILES et al.
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/748,875
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CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: 09/298,523
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
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33.1	33.3	33.3	33.4	33.5	33.6	33.6	33.7	33.7	33.8	33.9	34.0	34.2	34.3	34.3	34.4	
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	RESULT 1 G70218 G70218 G70218 C; Species: Borrelia burgdorferi (Lyme disease spirochete) C; Species: Borrelia burgdorferi (Lyme disease spirochete) C; Acte: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Ju1-2000 C; Accession: G70218; I40269; S37726; S70281 C; Accession: G70218; I40269; S37726; S70281 R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997 Nature 390, 580-586, 1997 A; Authors: Smith, H.O.; Venter, J.C.
nted,	A;Accession: G70218 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-210 <kle></kle>
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ce prot	
	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
	A; Residues: 1-210 <res></res>
ce prot	A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684 R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschek, E
	Med. Microbiol. Immunol. 182, 37-50, 1993 A;Title: Genetic heterogenity of the genes coding for the outer surface protein C (Os
	A;Reference number: S37726; MUID:93268136
	A;Status: preliminary
ce prot	A;Molecule type: DNA A;Residues: 1-210 <jau></jau>
	A;Cross-references: EMBL:X69596; NID:g311391; PIDN:CAA49306.1; PID:g311392
ce prot	R;Livey, I.; Gidds, C.P.; Schüster, K.; Dorner, F.
	A; Title: Evidence for lateral transfer and recombination in OspC variation in Lyme di
ce prot	A;Reference number: S/U255; MUID:96296448 A;Accession: S70281
	A;Status: nucleic acid sequence not shown
ce prot	A: Molecule type: DNA
	A;Cross references: EMBL:L42887; NID:g858715; PIDN:AAB36995.1; PID:g1695212
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A;Reference number: S72669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Variety: strain Pr
C; Date: 15-Feb-1997
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C:Species: Borrelia burgdorferi (Lyme disease spirochete)
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Residues: 1-124,'D',126-139,'E',141-210 <JAM>
Cross references: EMBL:X69589
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perfamily: Lyme disease spirochete surface protein C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
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86; Conservative
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Pred. No. 3.2e-36;
4; Mismatches 1
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Pred. No. 1.5e-36;
2; Mismatches 1; Indels
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A;Accession: I40129
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A;Molecule type: DNA
A;Residues: 1-177 <RES>
DTNN.
                                                                                              A;Gene: ospC
C;Superfamily:
                                                                                                                                                                                                 R.Thelsen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, J. Bacteriol. 177, 3036-3044, 1995
A.Title: Evolution of the Borrelia burgdorferi outer surface prote A;Reference number: I40104; MUID:95286481
                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                              outer surface protein C - Lyme disease spirochete (strain TXGW) (fragment) C:Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 02-Aug-196 #sequence_revision 02-Aug-196 #text_change 26-May-200; C:Accession: I40129; S54199
 Query Match
Best Local Similarity 98.9
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C:Superfamily: Lyme disease spirochete surface protein
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A;Accession: S70282
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 19-210 <LIV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U04281; NID:g434663; PIDN:AAC43297.1; PID:g434664 R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995 A;Title: Evidence for lateral transfer and recombination in OspC variation in A;Reference number: S70255; MUID:96296448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross references:
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Best Local Similarity 99.4
180; Conservative
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A/Title: Expression and sequence of outer surface protein C A/Reference number: 140143; MUID:95154673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-210 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLTSIDELAKAIGKK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLTSIDELAKAIGKK 79
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                                                                            Lyme disease spirochete surface protein
                                                                                                                  EMBL:X84783; NID:g793825; PIDN:CAA59254.1; PID:g793826
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De: strain 297
                        46.3%;
98.9%;
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Pred. No. 3.6e
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Pred. No. 2.
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                                  DB 2;
                      6e-33;
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.8e-34;
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                               Length 177;
Indels
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A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-193 <LIV>
A;Cross-references: EMBL:L42898; NID:g858729; PIDN:AAB3
A;Experimental source: strain 25015
C;GenetLcs:
A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
                                                                                                       outer surface protein C - Lyme disease spirochete C; Species: Borrella burgdorferi (Lyme disease spirochete) C; Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_C; Accession: S70279

R; Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995

A; Reference number: S7025; MUID:96296448

A; Accession: S70279
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C; Superfamily:
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A;Molecule type: DNA
A;Residues: 1-211 <RES>
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                                                                                                                                                                                                                                                                                                       KELTSPVVAESP 191
                                                                                                                                                                                                                                                                                                                               NKLKSSHTELGKQDAQDDDAKKAILRTHNTKDKGAEELDKLFKAVENLSKAAKEMLSNSV
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81.2%;
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Pred. No. 1.
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hes 22;
                                                        PIDN: AAB37007.1;
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                                                        PID:g1695223
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                                                                                                                                   Lyme
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    outer surface protein C precursor - Bot C; Species: Borrelia afzelii C; Date: 04-Sep-1997 #sequence_revision C; Accession: I40277 R; Fukunaga, M.; Hamase, A. J. Clin. Microbiol. 33, 2415-2420, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-193 <LIV>
A; Cross-references: EMBL:L42895; NID:g858723;
A; Cross-references: Strain 28354
                                                                                 RESULT
140277
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C;Superfamily: Lyme
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A;Title: Evidence for lateral transfer and reco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outer surface protein C - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-reb-1998 #sequence_revision 20-Feb-1998 #text_C;Accession: $70287
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A; Accession: S70287
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Best Local
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82.1%;
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76.3%;
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Pred. No. 1.1e-28;
""" tiematches 23;
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Pred. No. 6.4e-26;
6; Mismatches 28
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                                                                     Borrelia afzelii
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3 CNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIG
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                                                                                                                                                                 LEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKE
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                                                                                                                                                                                                                                                                                     CNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIG
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C;Superfamily: Lyme disease spirochete surface protein
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
A;Variety: strain pBre
C;Date: 06-Dec:-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000
C;Accession: 569918; S72674; T40103
R;Jauris-Heipke, S; Liegi, G; Preac-Mursic, V.; Roessler, D.; Schwab, E.; Soutschek, Elin. Microbiol. 33, 1860-1866, 1995
J. Clin. Microbiol. 33, 1860-1866, 1995
A;Title: Molecular analysis of genes encoding outer surface protein C (OspC) of Borrelia A;Accession: 569918
A;Accession: 569918
                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: S72674
                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: x81522;
                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-152, 'E', 154-211 < ROE>
                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A;Reference number: S72674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-211 <JAU>
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A;Residues: 1-211 <RES>
A;Cross-references: GB:D49501; NID:9707096; PIDN:BAA08461.1; PID:9769688
C;Superfamily: Lyme disease spirochete surface protein C
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A;Accession: 140277
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 37.1
Best Local Similarity 75.1
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              perimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oss-references: EMBL:x81522; NID:g872021; PIDN:CAA57242.1; PID:g872022
       120
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                                                                                                                             1 MACNUSGKDGNTSANSADESVKGPULTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 AIGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETF 118
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     NKLKEKHTDLGKEGVTDADAKEAILKTNGT-KTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                         IGKKIKNDGSLGDEANHNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS 135
                                                             IGKKIHQNNGLDTEXNHNGSLLAGAYAISTLIKQKLDGLK-NEGLKEKIDAAKKCSETFT 119
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                                                                                                              ISCNNSGKDGNTSANSÅDESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEL-AKA 75
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                                                                                                                                                                                                Conservative
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                                                                                                                                                                                       36.8%; Score 677.5; DB 2;
77.2%; Pred. No. 5.3e-25;
tive 11; Mismatches 30;
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75.1%;
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Pred. No. 2.8
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2.8e-25;
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                                                   Query Match
Best Local
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A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface
                                                   A;Cross-references: EMBL:L42871; NID:g858738; PIDN:AAB37014.1; PID:g1695229
A;Experimental source: Strain VS461
C;Genetics:
                                                                                                   A; Molecule type: DNA
A; Residues: 1-191 <LIV>
                                                                                                                                     A; Status: nucleic acid sequence
                                                                                                                                                       A;Reference number: S70255; MUID:96296448
A;Accession: S70278
                                                                                                                                                                                     R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination
                                                                                                                                                                                                                                                            outer surface protein C - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_
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A;Tittle: Outer surface protein C gene sequence analysis A;Reference number: I40269; MUID:96025162
A;Accession: I40273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Fukunaga, M.; Hamase, A.
J. Clin. Microbiol. 33, 24
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C;Date: 04-Sep-1997
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75.0%; Pred. No. 5.9e-25;
tive 20; Mismatches 25
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3 CNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIG

Similarity

36.6%; 75.8%;

Conservative

18;

Score 674.5; DB 2; Pred. No. 6.5e-25; 8; Mismatches 25;

Indels Length

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Gaps

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62

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Outer surface protein C precursor - Lyme disease spirochete C:Specles: Borrella burgdorferi (Lyme disease spirochete) C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 26-16;Accession: I40268

R:Margolls, N.; Hogan, D.; Cieplak, W.
Gene 143, 105-110, 1994

A:Title: Homology between Borrella burgdorferi OspC and members of 14, Reference number: I40268; MUID:94259285

A:Accession: I40268

A:Status: prellminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA, A:Residues: I-211 <RES>
A:Cross-references: GB:L25413; NID:g495735; PIDN:AAA22956.1; PID:g49C:Genetics:
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pression: I40153
pression: January B.P.; McHugh, G.L.; Leong, J.M.; Steere, A.C.
Infect. Immun. 62, 3213-3221, 1994
A;Title: Humora limmune response to outer surface pro-
pression: I40153; MUID:94314437
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C;Superfamily: Lyme disease spirochete surface protein
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A; Residues: 1-191 <RES>
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75.5%;
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RESULT
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outer surface protein C - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_C;Accession: S70277
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$70280
cuter surface protein C - Lyme disease spirochete c;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_
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C;Superfamily: Lyme disease spirochete
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Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and
A;Reference number: S70255; MUID:96296448
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C;Superfamily: Lyme
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74.5%;
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Pred. No. 8.1e-25;
                                                                                                                                                                                                                                                                                                                                                                        Score 672.5; DB 2;
Pred. No. 8.1e-25;
9; Mismatches 31;
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Lyme di

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R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.

Mol. Microbiol. 18, 257-269, 1995

A;Title: Evidence for lateral transfer and recombination in OspC variation in Lyme disea
A;Reference number: S70255; MUID:96296448
A;Accession: S70277
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-194 <LIV>
A;Residues: 1-194 <LIV>
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A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein C
Search completed: March 18, 2002, 09:56:46 Job time: 369 sec
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match 36.2%; Score 666; DB 2; Length 194; Best Local Similarity 74.3%; Pred. No. 1.6e-24; tches 142; Conservative 13; Mismatches 34; Indels
                                                                                                                                     181
                                                                                                                                                                      ELTSPVVAESP 191
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Maximum Match 100%
Listing first 45 s
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and is
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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2: /SIDSB/gcgdata,
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4: /SIDSB/gcgdata,
5: /SIDSB/gcgdata
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-	B. burgdorferi Osp			2501	Borrelia 297 antig	Borrelia B31 antig			B burgdorferi ospC	B31 outer surface	B. burgdorferi str	B31 Osp-A/antigen		lia IP2 (w	-	B31 outer surface	qs	Borrelia sp chimer	qs		qs	qs	qs	ds	g	sp	gp	sp		Borrelia sp chimer	S	Borrelia sp chimer

ALIGNMENTS

RESULT AAB62712 Chimeric - Borrelia sp. Chimeric - Borrelia sp. WPI; 2001-050113/06. N-PSDB; AAF29016. 03-APR-2001 (first entry) AAB62712 standard; Protein; 378 Dattwyler RJ, Seinost G, Dykhuizen D, (UYNY) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC. 18-JUN-1999; 99US-0140042 28-DEC-2000. WO200078966-A1. Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick Borrelia sp chimeric ospC protein SEQ ID NO: AAB62712; 19-JUN-2000; 2000WO-US16915 ⋛ Luft BJ, 28 Gomes-Solecki

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Dattwyler RJ,
                                                                                                                    Chimeric - Chimeric -
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Best Local (
                    (UYNY ) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
                                                                  19-JUN-2000;
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                                                 18-JUN-1999;
                                                                                  28-DEC-2000
                                                                                                  W0200078966-A1
                                                                                                                                         Borrelia; ospC; Lyme disease;
                                                                                                                                                                                                          AAB62738 standard; Protein;
                                                                                                                                                            Borrelia sp
                                                                                                                                                                             03-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Page 83-84; 160pp; English.
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                                                                                                                  Borrelia
Borrelia
                                                                                                                                                     chimeric ospC protein SEQ ID NO: 80.
                                                                2000WO-US16915
                                                                                                                                                                          (first entry)
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Pred. No. 2.9e-121;
0; Mismatches 0; Indels 0;
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 ВJ,
Gomes-Solecki
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Best Local
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                                  WO200078966-A1
                                                                                            Borrelia sp
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99US-0140042

RESULT

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19-JUN-2000; 2000WO-US16915
18-JUN-1999;
                                                                                                                                    Borrelia; ospc;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       122 LKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 43; Page 150-151; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compositions of OspC polypeptides from strains of Borrelia which caus Lyme disease are used to immunize animals and detect immune responses to Lyme disease -
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N-PSDB; AAF29042.
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                                                                                               Borrelia
Borrelia
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                                                                                                                                                     chimeric ospC protein SEQ ID NO:
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                                                                                                                                  Lyme disease;
                                                                                                                                                                                                                                    Protein;
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                                                                                                                                       Borrelia
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Lyme disease are used
to Lyme disease -
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      Borrelia sp
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Lyme disease are used
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DB; AAF29043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease;
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                                                                                                                                                                                                                                   Score 1589.5; DB 22;
Pred. No. 1.5e-102;
2; Mismatches 27;
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EIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKN
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Borrelia sp.
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Pred. No. 1.3e-100;
2; Mismatches 27;
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N-PSDB;
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Lyme disease are used
to Lyme disease -
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DB; AAF29033.
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       121
                                                                                                                                                                                                                   Claim 43; Page 91-92; 160pp; English.
                                                                                                                                                Sequence
                                                                                                                                                                                                                                          Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
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86.3%;
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                                                                                            Score 1528.5; DB 22; Pred. No. 2.3e-98; 0; Mismatches 31; ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 chimeric protein; tick.
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                                                                                             Indels
                                                                                                              Length 370;
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25

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Query Ma Best Loc Matches

Match

Local Similarity nes 326; Consert

82.1%; ilarity 86.0%; Conservative 1

11;

Score 1525.5; D Pred. No. 4e-98; 1; Mismatches

DB 31;

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394;

Indels Length

11;

Gaps

4;

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RESULT 1
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                                                      The present invention provides compositions comprising ospc protein chimeric ospc proteins from members of the Borrelia genus. These members of the Borrelia genus. These members of the Borrelia genus. These of Borrelia burgdorferi, B. afzelii or B. garinii. These can be used vaccines against Borrelia infection, which is spread by ticks and
  Sequence
                                                                                                                                                                                            Claim 43; Page 128-129; 160pp; English
                                                   to Lyme disease.
                                                                                                                                                                                                                                                  Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                    Dattwyler RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYNY ) UNIV NEW YORK STATE RES (BROO-) BROOK BIOTECHNOLOGIES IN
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Chimeric - Borrelia
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DB; AAF29034.
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                                                            leads
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62

Matches

Conservative

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Mismatches

33;

Indels

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Gaps

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357 361 297 82.0%;

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                                                                 Compositions of OspC |
Lyme disease are used to Lyme disease -
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Chimeric -
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                                                                                                                                                                                                                                Borrelia;
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                                                                                                                  Dattwyler RJ,
                                                                                                                               (UYNY ) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC.
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)B; AAF29030.
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Borrelia
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                                                                         s of Borrelia which detect immune respo
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                                                                                                                                                                                                                               protein;
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Query Match

80.

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Score 1496.5;

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22;

Length

The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea

leads anc be 3

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Lyme

disease.

Sequence

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Claim 43; Page 117-118; 160pp;

English.

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The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea
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                                                 Compositions of OspC |
Lyme disease are used
to Lyme disease -
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Chimeric -
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                                    Claim
                                                                               N-PSDB;
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DB; AAF29041.
                                    43; Page 147-148;
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                                                                                                                                                                                                                                                                                       standard;
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Borrelia
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                                                          from strains of Borrelia which cause animals and detect immune responses
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Best Local S
Matches 308
        Compositions of OspC polypeptides Lyme disease are used to immunize to Lyme disease -
                                                                                       (UYNY )
(BROO-)
                                            WPI; 2001-050113/06.
N-PSDB; AAF29022.
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                                                                                                                                                                                      Chimeric - Chimeric -
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                                                                                       UNIV NEW YORK STATE RES FOUND. BROOK BIOTECHNOLOGIES INC.
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                                                                     Dykhuizen D,
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Pred. No. 7e-96;
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               from strains of Borrelia which caus animals and detect immune responses
                                                                                                                                                                                                                chimeric
                                                                     Luft
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Best Local Similarity
Matches 311; Conserv
                                            (UYNY )
(BROO-)
WPI; 2001-050113/06
                      Dattwyler
                                                                                                   19-JUN-2000;
                                                                                                                                                                    Chimeric - Borrelia
Chimeric - Borrelia
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                                                                              18-JUN-1999;
                                                                                                                         28-DEC-2000
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to Lyme disease -
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                      19-JUN-2000; 2000WO-US16915
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        99US-0140042
                                                                                      Lyme disease;
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d to immunize animals and detect immune responses
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Pred. No. 2e-95;
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DB; AAF29028.
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                    KNLSKAAKEMLTNSVKEL
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                                                             KAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESV
                                                                                                                                                                                                                                                                                         al Similarity
309; Conserv
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211	209	193	211	194	201	212	190	194	203	201	212	203	202	193	211	201	191	191	201	209	212	211	194	211
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Q49577	044883	P94233	002507	031114	Q9RQR8	Q44727	P94244	P94247	050619	P96572	Q44705	050624	P96508	P94242	Q44976	P96573	P94245	Q44726	P96571	Q44671	Q9KIM5	Q44977	031122	Q49576
Q49577	044883	P94233	007607	nı.	Q9rqr8	Q44727	P94244	P94247	050619	P96572	Q44705	050624	P96508	P94242	Q44976	P96573	P94245	Q44726	P96571	Q44671	Q9kim5	Q44977	031122	Q49576
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Best Local S
Matches 188
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"Evidence for lateral transfer and re
Lyme disease Borrelia.",
Mol. Microbiol. 18:257-269(1995).
EMBL: 142887; AAB36995.1; -
EMBL: 142887; AAB36995.1; -
EMBL: Lipoprotein_6.
Pfold41; Lipoprotein_6. 1.
ProDom: PD001149; Lipoprotein_6; 1.
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Q9S3P3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-IP2;
                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; S
                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                   MEDLINE=96296448; PubMed=8709845;
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=139;
 123
                         61
                                                 63
                                                                         KEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL 182
                                      KKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL 122
                         KKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL
                                                                                                                              188;
                                                                                                                            Similarity 99.
88; Conservative
                                                                                                                                                                                          192
192 AA;
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20287
                                                                                                                                       50.3%;
                                                                                                                                                                                           MW;
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Spirochaetaceae; Borrelia
                                                                                                                              0,
                                                                                                                           Score 926; DB 2;
Pred. No. 2.1e-35;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                           Dorner F.; recombination
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183 180

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Query Match
Best Local Similarity
Matches 187; Conserv
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P70818;
01-FEB-1997
01-FEB-1997
01-JUN-2001
                                                                                    01-FEB-1997 (TIEMBLIE1. 02, Created)
01-FEB-1997 (TIEMBLIE1. 02, Last sequence update)
01-JUN-2001 (TIEMBLIE1. 17, Last annotation update)
0UTER SURFACE PROTEIN (FRAGMENT).
                                                 Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-TETS;

Marti-Ras N., Postic D., Foretz M.,
Submitted (MAR-1997) to the EMBL/Ge
EMBL; U91798; AABB1895.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
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MEDLINE-974/8003; PubMed-9336916;

Ras N.M., Postic D., Foretz M., Baranton G.;

"Borrella burgdorferi sensu stricto, a bacterial species 'made U.S.A.'?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-TER SURFACE PROTEIN C (PR. LENT)
00TER SURFACE PROTEIN C (PRAGMENT)
Borrella burgdorferi (Lyme disease spirochete)
Bacteria; Spirochaetales; Spirochaetaceae; Borrella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
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192 ‡
                                                                                                                                                                                                 PRELIMINARY;
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20297
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                        s disease spirochete).
Spirochaetaceae; Borr
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Pred. No. 3.5e-35;
2; Mismatches 1
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Best Local Similarity
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Best Local
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NON_TER
SEQUENCE
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Q9RR53;
Q1-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                             Wang I.N., Dykhuizen D.E., Qiu W., Dunn J.J., Bosler E.M., Lu Genetic diversity of ospC in a local population of Borrelia burgdorferi sensu stricto.";
Genetics 151:15-30(1999).
BMBL; AF02986; AAB86543.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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STRAIN=2-1498 CA4;

STRAIN=2-1498 CA4;

Probert W.S., Crawford M.R., Cadiz R.B., LeFebvre R.B.;

Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; L81131; AAB06569.1; -.

InterPro; IPR001800; Lipoprotein_6.

Pfam; PP01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99091544; PubMed=9872945;
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SEQUENCE
               61
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IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                          ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA
                                                                MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
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                                                                                                                                                                                                                                            193
193 AA;
                                                                                                                                   Conservative
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(TrembLrel. 13, Last sequence up)
(TrembLrel. 17, Last annotation
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98.9%;
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                                                                                                                                                       Score 908; DB 2; Pred. No. 1.3e-34;
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Pred. No. 1.1e-34;
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"Population dynamics of a naturally on
Borrella burgdorferi clones,";
Infect. Immun. 67:5709-5716(1999).
EMBL; AR074464; AAD23911.1;
InterPro; IPR001800; Lipoprotein_6.
Pfom; PF00141; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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O9R7B2 PRELIMINARY; PRT; 182 AA. 09R7B2; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) COTER SURFACE PROTEIN C (FRAGMENT). Borrelia burgdorferi (Lyme disease spirochete). Bacteria; Spirochaetales; Spirochaetaceae; Borrel
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Bacteria; Spirochaetales;
NCBI_TaxID=139;
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                                                        Wang I.-N., Dykhuizen D.E., Dunn J.J., Luft B. Submitted (OCT-1997) to the EMBL/GenBank/DDBJ EMBL; AF029869; AAB86552.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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Query Match 48.0%; Best Local Similarity 100.0%; Matches 181; Conservative

18.0%;

0;

Score 885; DB 2; Pred. No. 1.5e-33; 0; Mismatches 0;

Length 191;

Indels

0

Gaps

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RESULT
Q44719
ID Q4
AC Q4
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Q44719
Q44719;
01-NOV-1996
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NON_TER
NON_TER
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EMBL; L42893; AAB37001.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                       Q9S3P2 PRELIMINARY; PRT; 192 AA.
Q9S3P2;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2001 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CUTER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borr
                                                                    375
                                                                                  122
                                                                                                                                                                                                                                                                                               MEDLINE=96296448; PubMed=8709845;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=297;
                                                     182 S
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                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=139;
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                                                                                                                   IKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEFTAKLK 314
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192 /
(TrEMBLrel.
               PRELIMINARY;
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; 20472 MW;
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99.4%;
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 Created)
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               210
               AA
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.8e-33;
                                                                                                                                                                                                                                                                                                                                    Borrelia
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RESULT
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Stevenson B., Barthold S.W.;

**Expression and sequence of outer surface protein C repression is a sequence of outer surface protein C repression is a sequence of outer surface protein C repression is a sequence of outer surface protein. Texperate burgdorferi. Texperate burgdorferi. Texperate burgdorferi. Texperate burgdorferi. Texperate burgdorfering for the protein for the
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Best Local
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Q44999;
01-NOV-1996
01-NOV-1996
01-JUN-2001
                        NON_TER
                                                                              "Evolution of the Borrelia burgdorferi
J. Bacteriol. 177:3036-3044(1995).
EMBL; X84783; CAA59254.1;
Interpro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                              OSPC.
                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
OUTER SURFACE PROTEIN C (FRAGMENT).
                                                                ProDom; PD001149;
                                                                                                                                                                                    Hansen K.;
                                                                                                                                                                                                Theisen M., Borre
                                                                                                                                                                                                                                            STRAIN-TXGW,
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                     MEDLINE-95286481;
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi
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NCBI_TaxID=139;
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKNDVSLDNEADHNGSLISGAYLISTLITKKISAIKDSGELKAEIEKAKKCSEEFTAKLK 139
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180; Conservative
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177 i
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      ĀΑ;
                                                            Lipoprotein_6; 1.
49; Lipoprotein_6;
                                                                                                                                                                                              M., Mathiesen M.J.,
                                                                                                                                                                                                                     PubMed=7768799;
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99.48;
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17,
      MW;
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Spirochaetaceae;
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Last
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Pred. No. 3.1e-33;
0; Mismatches 1
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156671B9614E7A2D
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2D672991D584E4EE CRC64;
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                                                                                                                                                                                                                                                                                                                                     spirochete).
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                                                                                                                                                                                              Mikkelsen
                                                                                                                                                       outer surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                                                                                                                                                                                                                                                   Borrelia
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                                                                                                                                                       protein OspC.";
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Query Match

46.3%;

Score

853;

DВ

2.

Length 177;

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RESULT
Q9REH7
ID Q9
AC Q9
                        RESULT
Q9R7B4
ID Q9
AC Q9
AC Q9
DT 01
DT 0
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Best Local Similarity
Matches 175; Conserv
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O9R7B4 PRELIMINAL,
O9R7B4;
O9R7B4;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update
O1-JUN-2001 (TrEMBLrel. 17, Last annotation upda
OUTER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
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O9REH7;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theisen M., Frederiksen B., Lebech A.M., Vuust J.,
"Polymorphism in ospC gene of Borrelia burgdorferi
immunoreactivity of OspC protein: implications for
use of OspC protein as a diagnostic antigen.";
J. Clin. Microbiol. 31:2570-2576(1993).
EMBL; X73622; CAA52001.1;
InterPro; IPR001800; Lipoprotein_6.
pfam; PF01441; Lipoprotein_6; 1.
ProDom: PD001149; Lipoprotein_6; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-B31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Spirochaetales;
NCBI_TaxID=139;
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                                                                                                                                                                                                                                                                                                                    GKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVV
                                                                                                                                                                                                                                                                                                                                          GKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVV
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178 t
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18894
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98.3%;
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. 13, Last sec
. 17, Last and
C (FRAGMENT).
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Pred. No. 1e-3
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 17, Last sequence update
01-JUN-2001 (TrEMBLrel. 17, Last annotation update
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria: Spirochaetales; Spirochaetaceae; Borre
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                                                                                                                                             InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                Marti-Ras N., Postic D., For Submitted (MAR-1997) to the EMBL; U91801; AAB81898.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9R7A9;
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[2]
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"Borrelia burgdorferi sensu
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167; Conservative
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175 AA;
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Pred. No. 4.5e-31;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
01-JUN-2001 (TREMBLREL 17, Last annotation updat
0UTER SURFACE PROTEIN C (FRAGMENT).
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01-JUN-2001
01-JUN-2001
01-JUN-2001
SEQUENCE FROM N.A. STRAIN-TETS;
                          Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; SNCBI_TaxID=139;
                                                                                                        Q9R7B0
                                                                                                                                                                                                                                                                                                                                         disease spirochete, Borrelia EMBO J. 0:0-0(2001).
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Lawson C.L., Swaminathan S.;
"Crystal structure of outer surface protein original structure, Borrelia burgdorferi.";
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(TremBLrel. 17, Last seq
(TremBLrel. 17, Last ann
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                                   Spirochaetaceae; Borrelia.
                                               disease
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Spirochaetaceae; Borrelia
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Pred. No. 3.7e-29;
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U91799; AAB81896.1; -
InterPro; IPR001800; Lipoprotein_6.
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Copyright GenCore version 4.5 (c) 1993 - 2000 Comp Compugen Ltd

OM protein - protein search, using sw model

9 March 18, 2002, 09:55:42; Search time 39.62 Seconds (without alignments)
347.030 Million cell updates/sec

Title: Perfect score: US-09-596-746A-24. 1842

Sequence: MACNNSGKDGNTSANSADES... KNLSKAAKEMLTNSVKELTS

Scoring table: BLOSUM62 Gapop 10. 10.0,

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OUTER SURFACE PROTEIN C PRECURSOR (PC)
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Pfam; PF01441; Lipoprotein_6; 1.

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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Signal; Plasmid; Antigen;
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burgdorfori.";
Nature 390:580-586(1997).
Nature 390:580-586(1997).
-i- FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.
-i- FUNCTION: ATTACHED TO THE OUTER MEMBRANE
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Plasmid.
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                                     NCBI_TaxID=140;
                                                        Bacteria;
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J. Clin. Microbiol. 31:2570-2576(1993).
-!- FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE
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Best Local
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01-JUL-1993 (Rel. 26, L
01-FEB-1994 (Rel. 28, L
VARIABLE MAJOR OUTER ME
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SEQUENCE
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STRAIN-SSP. HS1 SEROTYPE 3;
MEDLINE-93133110; PubMed-1484486;
Restrepo B.I., Kitten T., Carter '
"Subtelomeric expression regions
                                                                             SEQUENCE FROM N.A
STRAIN-SSP. HS1 SI
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Mol. Microbiol. 6:3299-3311(1992).
                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                Plasmid
                                                                                                                                                                                                                       Borrelia hermsii
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                                                                                                                                              NCBI_TaxID-140;
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Pred. No. 3.
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VARIABLE MAJOR OUTER MEMBRANE
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  C.J., Infante D., Barbour A.G. of Borrelia hermsii linear pla
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Best Local S
Matches 94
Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.;

"Complete nucleotide sequence and deduced polypeptide sequence nonmuscle myosin heavy chain gene from Acanthamoeba: evidence o hinge in the rodilke tail.";

J. Cell Biol. 105:913-925(1987).

-I- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS A ACTIVATTY THAT IS ACTIVATED BY F-ACTIN.

-I- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEM INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Plasmid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are highly polymorphic.";
Mol. Microbiol. 6:3299-3311(1992).
-i- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=87308395;
                                                                                                                                                                            MYOSIN II HEÀVY CHAIN, NON MUSCLE.
Acanthamoeba castellanii (Amoeba).
Eukaryota; Acanthamoebidae; Acanthamoeba.
NCBI_TaxID-5755;
                                                                                                                                                                                                                                        01-NOV-1988 (Rel. 20-AUG-2001 (Rel.
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01-NOV-1988
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Pred. No. 5e-12;
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N-ACYL DIGLYCERIDE
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VARIABLE MAJOR OUTER MEMBRANE
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Best Local S
Matches 103
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InterPro; IPRO00048; IQ.
InterPro; IPRO01609; myosin_head.
Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
PRINTS; PRO0193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
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MOD_RES
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MOD_RES
SEQUENCE
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PROSTIE; PS50096; IQ; 1.

Myosin; Colled coll; Actin-binding; ATP-binding; Calmodulin-binding; Myosin; Colled coll; Actin-binding; Multigene family.

Methylation; Alkylation; Phosphorylation; Multigene family.

MYOSIN HEAD-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                       OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A27224; A27224.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y00624; CAA68663.1;
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or send an email to license@isb-sib.ch)
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                                                                                                                                                               78
                                                                                                                                                                                                                       28
VDSLKSKLSAAEKSL--KTAKDQNRDLDEQLEDERTVRANVDKQKKALEAKLTELEDQVT
                                                           RNELDDVTATKLQLEKTKKSLEEELAQTRAQLEE-EKSGKEAASSKAKQLGQQLEDARSE
                                                                                    TDA--DAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE------
                                   ---LTSPVVAESPAMVNNSGKDGN-----
                                                                                                                                                    NGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDA---AKKCSETFTNKLKEKHTDLGKEGV
                                                                                                                                                                                                            EISKKITDSNAVLLAVKEVEA----LLSSIDE-----IAAKAIGKKIHQNNGLDTEYNH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NON-HELICAL TAILPIECE WHERE THE REGULATORY PHOSPHORYLATION SITES RESIDE.

MISCELLANDOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTIVITY. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 2 IQ DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

[MLC-2]

[DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDE: CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00015; IQ; 1.
SM00242; MYSC;
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                       1489
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766
133
700
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848
848
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                                                                                                                                                                                                                                                                                                                         171201 MW;
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                                                                                                                                                                                                                                              Score 176.5; DE 
Pred. No. 0.41; 
68; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                               METHYLATION (TRI-)
ALKYLATION (SH-1) (
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COILED COIL (POTENTIAL).
ALPHA-HELICAL TAILPIECE
                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPHA-HELICAL TAILPIECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIGHT MEROMYOSIN (LMM)
                                                                                                                                                                                                                                                                                                                      2CE49BE51173D17E CRC64;
                              -TSANSADESVKG--PNLTEISKKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                               137;
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                                                                                                                                                                                                                                                                         Length 1509;
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Best Local
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01-APR-1993
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                          or send
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Q00799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=92315338; PubMed=1617731;
Galinski M.R., Medina C.C., Ingra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ol-ARR-1993 (Rel. 25, Created)
Ol-ARR-1993 (Rel. 25, Last sequence update)
Ol-CCT-1996 (Rel. 34, Last annotation update)
RETICULOCYTE BINDING PROTEIN 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A reticulocyte-binding protein complex of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1261 LERLEBELLTAQEARAAAEK-NLDKAN--LELEBLRQEADDAARDNDKLVKDNRK 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium vivax (strain Belem)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1161 ALDGQKNA----AAAQAKTLKTQVDETKRRLEEAEASAARLEKERKN---ALDEVAQ-----
                                                                                                                                                                08
                                                                                                                                                                                                      22 KGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA--IGKKIHQNNGLDTEYNHNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226
                                      KTLEGEVNA---
                                                                                                                                                        SLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL---KEKHTDLGKEGVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 69:1213-1226(1992).
FUNCTION: INVOLVED IN RETICULOCYTE ADHESION.
HUMAN RETICULOCYTE CELLS.
                                                       KELTSPVVAESPAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVET
                                                                                  KSYDNIIALEKQTELQNLRNSFTQEKTNTNSDSKLEKIKTDFES
                                                                                                                                ----YLKVVLINQ-----YKNKISSIKSKEEAVSVKIGNVSKKHSELSKITCSD
                                                                                                                                                                                KNTNELDVHKNIQDAYKVALEI-----LAHSDEIDTKQKDSSKLIEMGNQI-----
                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ESNAVVLAVKEVETLLTSIDEL------AKAIGKKIKNDVSLDNEADHNGSL
                                                                                                                                                                                                                                       93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISGAYLISNLITKKISAIKDSG-----
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    Receptor; Membrane.
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1251 AA;
                                                                                                                                                                                                                                    Conservative
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                               ---LKASSDNHEHVQSKSEPV-NPALSEIEKEET------DIDS
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                                                                                                                                                                                                                                                9.2%;
                                                                                                                                                                                                                                                                                                 143741 MW;
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-AIGKKIKNDVSLDNEADHNGSLISGAYL---
                                                                                                                                                                                                                                               Score 170;
Pred. No.
                                                                                                       KTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSV
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                                                                                                                                                                                                                                                        Length 1251;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 222.8 KDA PROTEIN C1F3.06C IN CH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical SEQUENCE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Connor R., Churcher C.M., Submitted (APR-1996) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-972;
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Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPACIF3.06C.
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                                                                                                                                                                                                                                                                             DKMVKQVSSQLEEARSSLAHATGKLAEINSERDFQNKKIKDFEKIEQDLRACLNSSSNEL
                                                                                                                                                                                                                                                                                                                                                                       KDGNTSANSADE - - - SVKGPNLTEISKKITDSNAVLLAV - KEVEALLSSIDEI - - - - -
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KISAIKDSGELKAEIEKAKKCS----EEFTAKLKGEHTDLGKE----
                                                                                                                      LANSVKELTSPVVAESPAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESN-AVVLA
                                                                                                                                                    LKGELQTEISNSEHLSSQLSTLAAEKEAAVATN-
                                                                                                                                                                                                                 KEKSALIDKKDQELNN--LREQIKEQKKVSESTQSSLQSLQRDILNEKKKHEVYESQLNE
                                                                                                                                                                                                                                             ---STLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL--
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                                                           VKEVETLLTSIDELAKAIGKKIKNDVSLDNE-----ADHNGSLISGAYLISNLITK
                            LKDTSSKLOOL-OLERANFEOKESTLSDENNDLRTKLLKLEESNKSLIKKOEDVDSL-EK
                                                                                       LAKSVMQL-----KENEQNFSSLDTSFK--KLNESHQELENNHQTITKQ
                                                                                                                                                                                                                                                                                                                                                                                                     107;
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l protein.
1957 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                  ----TDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEM
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                                                                                                                                                                                                                                                                                                                                                                                                                9.2%;
23.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 169;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                      ---NELSESKNSLQTLCNAFQEK
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                                                                                                                                                                                                                                                                                                                                                                                                     156;
                                                                                                                                                                                                                                               ----KEKH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1957;
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RESULT
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01-AUG-1988
20-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDILIND=86111835; PubMed=3511046;
Hollingshead S.K., Fischetti V.E., Scott J.R.;
Hollingshead S.K., Fischetti V.E., Scott J.R.;
"Complete nucleotide sequence of type 6 M protein of the
Streptococcus. Repetitive structure and membrane anchor."
J. Biol. Chem. 261:1677-1686(1986).
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long a
modified and this statement is not removed:
entitles requires a license agreement (See i
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc.
                           DOMAIN
                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                   InterPro; IPR001899;
InterPro; IPR003345;
                                                                                                                                                                                                                                                                               EMBL; M11338; AAA26920.1; PIR; A26297; A26297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scott J.R., Pulliam W.M., Hollingshead S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 43-122 FROM N.A. MEDLINE=85166224; PubMed=3885219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pyogenes
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                                                                                                                         DOMAIN
                                                                                                                                                     SIGNAL
                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                        Pfam; PF00746; Gram_pos_anchor; Pfam; PF02370; M; 9.
                                                     DOMAIN
                                                                    DOMAIN
                                                                                  DOMAIN
                                                                                                                                                                                 Virulence; Phagocytosis;
                                                                                                                                                                                              PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Relationship
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            750 L--SSELTKSSEDVKRLTANVETLTQDSKAMKQSFTSLVNSYQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: TYPE I MEMBRANE SIMILARITY: TO OTHER M PROTEINS. SIMILARITY: TO OTHER STREPTOCOCCAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tt J.R., Pulliam W.M., Hollingshead S.K., Fischetti V.A.; lationship of M protein genes in group A streptococci."; c. Natl. Acad. Sci. U.S.A. 82:1822-1826(1985).
FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SEROTY! OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: TO OTHER M PROTEINS.
SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT
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8 (Rel. 08, Last sequence up
1 (Rel. 40, Last annotation
SEROTYPE 6 PRECURSOR.
                                                     157
279
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457
477
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138
269
347
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                                                                                                                                                                                                                                                                Gram_pos_anchor
                                                                                                                                                                   coil;
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                                                                                                                                                                                 Cell wall;
                                                                                                                                                                 Signal
GLY/PRO-RICH
CONSERVED IN
                                                    4.5 x 25 AA TANDEM REPEATS
TWO DIRECTLY REPEATED 27 A
                                                                                  10
                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                         M PROTEIN, SEROTYPE 6.
EXTRACELLULAR (POTENTIAL).
                           HYDROPHILIC
                                        BLOCKS SEPARATED BY
                                                                                                            MEMBRANE ANCHOR
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                                                                                 7 AA TANDEM REPEATS
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(CELL WALL-SPANNING).
GRAM-POSITIVE COCCI SURFACE
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                                        15
                                                                                                                                                                                 Repeat;
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RESULT 9
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Best Local
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                                                                                                                                                                                                                                                                                                         P19401;
P19401;
P19401;
P19401;
P19401;
P1950 (Rel. 16, Last sequence update)
P1950 (Rel. 16, Last anotation update)
P1950 (Rel. 40, Last anotation update)
P1950 (Rel. 40, Last anotation update)
P1950 (FRAGMENT).
                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-CS24 / Serotype M12;
MEDLINE-88058777; PubMed-2445730;
Robbins J.C., Spanier J.G., Jones S.J., Simpson W.J., Clear
                modified and
                                                               This
         entities
                             use
                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Streptococcus.
                                       the European
                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes.
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                                                                                                                                                                                                                                                                      NCBI_TaxID=1314;
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                                                                                                                                      Bacteriol. 169:5633-5640(1987).

- FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SEROTYPES OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE OF THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
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                                                                                 SUBCELLULAR LOCATION: TYPE I MEMBRANE P
SIMILARITY: TO OTHER M PROTEINS.
SIMILARITY: TO OTHER STREPTOCOCCAL AND
IN THE REGION OF THE MEMBRANE ANCHOR.
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SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way fied and this statement is not removed. Usage by and for commercial ties requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                   PHAGOCYTOSIS.
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Pred. No. 0.31;
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68F87F28DB53A448
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                                                                                                                   PROTEIN. CELL WALL
                                                                                             STAPHYLOCOCCAL PROTEINS
                                                                                                                                                                                                                                                                                        group; Streptococcaceae;
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  NCBI_TaxID=4932;
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Query Match
Best Local
            USO1_YEAST STANDARD; PRT; 1790 AA.
P25386;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1
USO1 OR INTI OR YDLO50W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycetes;
   Saccharomycetales;
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SEQUENCE
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DOMAIN
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Virulence; Phagocytosis; Cell wall; Duplication; Repeat; Antigen;
Transmembrane; Coiled coil; Signal.
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SIGNAL
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InterPro; IPR003345; M_repeat.
Pfam; PF00746; Gram_pos_anchor; 1.
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EMBL; U53668; AAB66659.1; -.
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Submitted (MAY-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A cytoskeleton-related gene, usol, protein transport in Saccharomyces of Cell Biol. 113:245-260(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hostetter M.K., Herman D.J., Kendrick K.E.;
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SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
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DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE,
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G -> E (IN REF. 2).

E -> K (IN REF. 2).

V -> I (IN REF. 2).

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PROTEIN TRANSPORT FROM THE ER
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73; Mismatches
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p49454; Q13246; Q13171;
01-FEB-1996 (Rel. 33, Create
01-FEB-1996 (Rel. 33, Last s
20-AUG-2001 (Rel. 40, Last a
CENP-F KINETOCHORE PROTEIN (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Breast carcinoma;

MEDLINE-95348175; PubMed=7542657;

Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;

"CENP-F is a protein of the nuclear matrix that assembles onto kinetochores at late G2 and is rapidly degraded after mitosis.";

J. Cell Biol. 130:507-518(1995).
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Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                               SEQUENCE OF 2194-3210 FROM N.A.

MEDITINE-95336446; PubMed-7612011;

Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., i.

"A novel cell-cycle-dependent 350-kDa nuclear protein:
domain sufficient for nuclear localization.";

Biochem. Biophys. Res. Commun. 212:220-228(1995).
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CHARACTERIZATION.
MEDLINE=98437347; PubMed=9763420;
Chan G.K.T., Schaar B.T., Yen T.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that is specifically involved in mitotic-phase Mol. Cell. Biol. 15:5017-5029(1995).
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J. Cell Biol. 143:49-63(1998).

-I- FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION, INVOLVED IN CHROMOSOME SEGRECATION DURING MITOSIS. INTERACTS WITH RETINOBLASTOMA PROTEIN (RB), CENP-E AND BUBRI.

-I- SUBGUNIT: HOMO- OR HETERODIMER.

-I- SUBCELIULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE NUCLEOLUS), REORGANIZATION TO THE KINETOCHORE/CENTROMERE (CORONAL SURFACE OF THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS.

-I- DEVELOPMENVAL STAGE: GRADUALLY ACCUMULATES DURING THE CELL CYCLE.
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V -> A (IN REF. 2).
V -> L (IN REF. 2).
ER -> DG (IN REF. 3).
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X-RAY CRYSTALLOGRAPHY (2.1 MEDLINE=97452580; PubMed=9.
                                "X-ray structure of the magnesium(II). Dictyostellum discoideum myosin motor Biochemistry 35:5404-5417(1996).
                                                                                                                                Smith C.A., Rayment I.;
"X-ray structure of the magnesium(II)-pyrophosphate complex of the "runnated head of Dictyostelium discoldeum myosin to 2.7-A
                                                                      MEDLINE=96206189;
Smith C.A., Rayme
                                                                                                                                                                                                                "X-ray structures of the myosin motor discoideum complexed with MgADP.BeFx Biochemistry 34:8960-8972(1995).
                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
MEDLINE=95345067; PubMed=7619796;
                                                                                                                    Biochemistry 34:8973-8981(1995).
                                                                                                                                                                                                                                                                                                              Wagle G., Noegel A., Scheel J., Gerisch G. "Phosphorylation of threonine residues on Dictyostelium myosin heavy chain."; FEBS Lett. 227:71-75(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1988
01-OCT-1989
20-AUG-2001
                                                                                             X-RAY CRYSTALLOGRAPHY (1
                                                                                                                                                                                                                                                               Fisher A.J., Smith C.A., Thoden J.B.,
                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 1-762
MEDLINE=95345066; PubMed=7619795;
                                                                                                                                                                                                                                                                                                                                                                                           phosphorylatable heavy chain fragment of Dictyostelium myosin FEBS Lett. 269:239-243(1990).
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88112226;
                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION SITES
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Lueck-Vielmeter D., Schleicher M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-AX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1988 (Rel. 09, 01-OCT-1989 (Rel. 12, 120-AUG-2001 (Rel. 40, 140-140) MYOSIN II HEAVY CHAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION SITES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium
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Conserved protein domains in a myosin heavy
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                                                                        Rayment
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                                                                                APHY (1.9 ANGSTROMS)
Pubmed=8611530;
 PubMed=9305951;
                                                                                                                                                                                                                                                                                                                                                              PubMed=2828113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=3540939;
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                                                                                                                                                                                                                                         motor
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                                                                                                                                                                                                                           r domain of Dictyostelium
and MgADP.AlF4-.";
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           OF 1-762
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                                                                                                                                                                                                                                                               Smith R.,
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                                             1.9-A resolution.";
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DR COR
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PIR: S00250; S00250.

PIR: S00250; S00250.

PDB: 1MMD; 17-AUG-96.

PDB: 1MMD; 17-AUG-96.

PDB: 1MND; 17-AUG-96.

PDB: 1MND; 17-AUG-96.

PDB: 1VOM; 23-DEC-96.

PDB: 1LVK; 28-JAN-98.

PDB: 1LVK; 28-JAN-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "X-ray crystal structure and solution fluorescence characterization of Mg.2'(3')-O-(N-methylanthraniloy!) nucleotides bound to the Dictyostelium discoideum myosin motor domain.";

J. Mol. Biol. 274:394-407(1997).

-I- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY ACTIN.

SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEAVY ENAIN IS TWO-HEADED. TO SELF-ASSEMBLES INTO FILAMENTS. HEAVER OF 2 HEAVY CHAIN SUBUNITS (MIC), 2 ALKAL LIGHT CHAIN SUBUNITS (MIC), 3 ALKAL LIGHT CHAIN SUBUNITS (MIC)
     NP_BIND
DOMAIN
DOMAIN
MOD_RES
                                                                                                                                                                                                                       SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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"X-ray structures of the MgADP, MgATPgammaS, and MgAMPPNP complexes of the Dictyostellum discoideum myosin motor domain.";
Biochemistry 36:11619-11628(1997).
                                                                                                                                                                                                     Myosin; Coiled
                                                                                                                                                                                                                                                                                            PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M14628; AAA33227.1; PIR; A26655; A26655.
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                                                                                                      DOMAIN
                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROMYOSIN (LMM) AND 1 HEAVY MEROMYUSIN (FIRM).

SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

SUBFRAGMENT (S2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION AND REDUCES THE ACTIN-ACTIVATED ATPASE ACTIVITY.

MISCELLAMEOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EDTA ATPASE ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE OF A CYS AT THE SH-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD SIMILARITY: CONTAINS 1 IQ DOMAIN.
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DOMAIN: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT II

MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MLC-2).
SUBCELLULAR LOCATION: HIGHEST CONCENTRATION IN THE POSTERIOR CELL
                                                                                                                                                                                                                                                                                                                                             PF00612; IQ; 1.
PF00063; myosin_head; 1.
       762
817
179
638
738
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     761
791
2116
186
660
752
130
                                                                                                                                                                         Actin-binding; ATP-binding; 3D-structure Methylation; Alkylation; Phosphorylation
ATP.
ACTIN-BINDING.
ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (DI-) (POTENTIAL).
                                                                                                 IQ.
COILED COIL
                                                                                                                                                    HEAD-LIKE
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RRITH RAY
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SEQUENCE
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                                                                                                       Sasaki M., Kato S., Kohno K., Martin G.R., Yamada Y.; "Sequence of the cDNA encoding the laminin B1 Chain r multidomain protein containing cysteine-rich repeats. proc. Natl. Acad. Sci. U.S.A. 84:935-939(1987).
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                                 "Sequencing of laminin B chain coiled-coil alpha-helix.";
                                                                   SEQUENCE OF 1292-1786 FROM N.A. MEDLINE-85051302; PubMed-6209134;
                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=87147212; PubMed=3493487;
                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                       LAMININ BETA-1 CHAIN LAMB1-1 OR LAMB-1.
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SEQUENCE
                                                         Barlow D.P., Green N.M.,
                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                            LMB1_MOUSE
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OF 165-172; 539-547
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1823
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6 AA;
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1833
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Rodentia;

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Sciurognathi;
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                                                          Hogan B.L.M.;
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thi; Muridae;
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; Murinae; Mus
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MGD; MGI:96743; LambI-1.

MGD; MGI:96743; LambI-1.

InterPro; IPR000561; EGF-like.

InterPro; IPR001886; LamMY.

InterPro; IPR002049; Laminin_EGF.

Pfam; PF00053; laminin_EGF; 13.

Pfam; PF00055; laminin_Meerm; 1.

PRINTS; PR00011; EGFLAMININ.

PRODOM; PD002082; LamNT; 1.

SMART; SM00180; EGF_Lam; 11.
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SMART; SM00136; LamWT; 1.
PROSITE; PS00022; EGF_1; 9.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ.TYPE_EGF; 11.
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Laminin EGF-like domain; Cell ad
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EMBL; X05212; CAA28839.1;
PIR; A26413; MMMSB1.
HSSP; P03069; 1ZIM.
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"Cloning of the mouse laminin alpha 4 cDNA. Expression endothelium.";
Eur. J. Biochem. 246:727-735(1997).
-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECE
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SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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"Phylogenetic analysis of Rickettsia spp. by comparing sequence 'Phylogene D' coding for an intracytoplasmic protein.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-I- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
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                                                                                                                                      Antigen.
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                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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Rickettsiaceae; Rickettsie
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103 HEAT-STABLE 120 KDA PROTEIN (PS120)
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P24733;
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"Complete primary structure of a scallop striated muscle myosin chain. Sequence comparison with other heavy chains reveals regio that might be critical for regulation.";
J. Biol. Chem. 266:18469-18476(1991).
Nature [4]
                                                                                                                      Nyitray L., Goodwin E.B., Szent-Gyorgyi A.G.;
"Nucleotide sequence of full length cDNA for
muscle myosin heavy chain.";
nucleic Acids Res. 18:7158-7158(1990).
                                                                                                                                                                                                                                                                                                    TISSUE-Adductor muscle; meDLINE-92011595; pubMed-1917970;
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                            resolution.
                               Szent-Gyorgyi A.G., Cohen C. "Structure of the regulatory resolution.":
                                                                Xie X., Harrison D.H., Schlichting I.,
                                                                              x-ray Crystallography (2.8 ANGSTROMS) OF MEDLINE-94173332; PubMed-8127365;
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InterPro; IPRO002928; Myosin_tail.
InterPro; IPRO02928; Myosin_tail.
InterPro; IPRO02017; Spectrin.
InterPro; IPRO01609; myosin_head.
Pfam; PP00612; IQ; 1.
Pfam; PP0063; myosin_head; 1.
Pfam; PP01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
SMART; SM00215; IQ; 1.
SMART; SM00215; IQ; 1.
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1037 REKKVRGDVEKA-----KRKVEQDLKSTQENVEDLERVKRE-LEENVRRKEAEI---- 1084
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Myosin; Muscle proteir
ATP-binding; Alkylatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIAMOC
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-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC). 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
-!- SUBCELLUAR LIGHT CHAIN SUBUNITS (MLC-2)
-!- SUBCELLUAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                               74 ---EYNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTNKLKEKHTDLG 130
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PDB; 1WDC; 11-JUL-96.
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Structure 4:21-32(1996).
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US-08-29-603E-15
US-09-196-293-15
US-08-235-836C-107
US-08-235-836C-107
US-08-158-353-2
US-08-158-353-2
US-08-158-353-4
US-08-158-353-4
US-08-158-353-4
US-08-235-836C-34
US-08-235-836C-34
US-08-235-836C-34
US-08-235-836C-36
US-08-235-836C-36
US-08-235-836C-36
US-08-353-836C-36
US-08-353-700-1
US-08-353-700-1
US-08-685-576-1
US-08-685-576-1
US-08-685-576-4
US-08-125-077-4
US-08-125-077-4
US-08-125-077-4
US-08-125-077-4
US-08-125-077-4
US-08-141-121-4
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Compugen Ltd
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Sequence 110, App Sequence 15, Appl Sequence 15, Appl Sequence 122, Appl Sequence 127, Appl Sequence 27, Appl Sequence 28, Appl Sequence 29, Appl Sequence 31, Appl Sequence 36, Appl Sequence 36, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 19, Appl Sequence 1
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1 MACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDETAAKA 60

Query Match
Best Local Similarity 59.5
Matches 229; Conservative

52.1%; 59.5%;

32;

Score 968.5; DB 4; Pred. No. 5.2e-62; 2; Mismatches 93;

Indels 31;

Gaps

Query Match 52.1%; Score 968.5; DB 4; Best Local Similarity 59.5%; Pred. No. 5.2e-62;	ic Prots and U ory.	28 144.5 7.8 1164 4 US-08-923-992A-2 29 144 7.7 1713 3 US-08-600-982-24 30 144 7.7 1713 5 PCT-US94-10261A-24 31 143 7.7 630 4 US-08-973-462-9 32 142.5 7.7 1164 4 US-08-923-992A-10 34 142 7.6 1507 3 US-08-923-992A-10 35 139.5 7.5 1588 5 PCT-US93-07261-11 36 139.5 7.5 1663 5 PCT-US93-07261-16 37 138 7.4 641 4 US-08-923-992A-8 41 135.5 7.3 1038 4 US-08-921-982A-6 42 135.5 7.3 1128 4 US-08-921-922A-6 43 134 7.2 3128 4 US-08-923-992A-6 44 132 7.1 1561 3 US-08-923-992A-6 45 131.5 7.1 1561 3 US-08-93-992A-6 46 135.5 7.3 1128 4 US-08-923-992A-6 47 135.5 7.3 1128 4 US-08-923-992A-6 48 132 7.1 1561 3 US-08-93-992A-6 49 135.5 7.3 1128 4 US-08-93-992A-6 40 135.5 7.3 1128 4 US-08-93-992A-6 41 135.5 7.3 1128 4 US-08-93-992A-6 42 135 7.3 128 4 US-08-93-992A-6 43 134 7.2 376 5 5180810-1 44 132 7.1 1561 3 US-08-93-017-23 45 131.5 7.1 695 1 US-08-127-49A-23
Length 466;	eins Comprising	Sequence 2, Appli Sequence 24, Appl Sequence 9, Appli Sequence 10, Appli Sequence 15, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 160, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 17, Appli Sequence 17, Appli Sequence 23, Appli Sequence 23, Appli

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, MOLECULE TYPE: US-08-158-353-3
                                  Best Local Similarity 97.
Matches 190; Conservative
                                                                 Query Match
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; Sequence 3, Application US/08158353
; Patent No. 5620862
; GENERAL INFORMATION:
                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: CAITCIL, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UCT93-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                           TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
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                                                                                                                                                                                                                                                                                                                                 COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIF: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Mil:
CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hamilton, Brook, Smith & Reynolds, p.c. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 TAEKTTLVVKEGTVTLSKNISKSGE 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 SAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGAD 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 KLELKGTSDKNNGSGVLEGVKADKSKVKLTIS----DDLGQTTLEVFKEDGKTLVSKKV 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVETLLTS-----IDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLI--SNLITKKI 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELTSPYVAESPKKPKQ-NVSSLD---EKNSVSVDLPGEMKVLVSKEKNKDGKYDLIATVD 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELTSPVVABSPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKTTESNA--VVLAVK 238
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                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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VENTION: Methods for Diagnosing Early Lyme
                                                                                                                  protein
                                                                                                                                           single
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                                            50.8%;
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                       Score 945; DB 1;
Pred. No. 8.9e-61;
3; Mismatches 1
                                              Length 210;
                      Indels
                   0;
                 Gaps
              0
                                                                                                                                                    PRIOR APPLICATION: 436

APPLICATION NUMBER: PCT/EP90,
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/862
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR--
TELEPHONE: (212) 697-335
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                MOLECULE TYPE:
DESCRIPTION: PROTEIN
HYDOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: N/A
ORIGINAL SOURCE: N/A
ORIGINAL SURCE: B. BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-08-209-603E-15
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           ORGANISM: B. E
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Patent No. 6248538
GENERAL INFORMATION:
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MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version
SOFTMARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                  TYPE: AMINO ACID
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MOTZ, MANFRED
APPLICANT: SOUTSCHECK, ERWIN
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE: 10-MAI
CLASSIFICATION: 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
CITY: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 ELTSPVVAESPKKP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGABELGKLFESVEVLSKAAKEMLANSVK 180
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DSM 5662
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WILSKE, BETTINA
PREAC-MURSIC, VERA
                                                                                                                                                                                                                                                                                                                                                       JMBER: US/08/209,603E
10-MAR-1994
                                                                                                                                                                                                                                                                                                               PCT/EP90/02282
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RESULT 4
US-09-196-293-15
; Sequence 15, Applic
; Patent No. 6183755
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettins
APPLICANT: Wilske, Bettins
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.0010S2
CURRENT APPLICATION NUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-10-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IDENTIFICATION METHOD: ; PUBLICATION INFORMATION: US-08-209-603E-15
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                                                                                                                                                                                                                                   ; ORGANISM: Borrelia burgdorferi US-09-196-293-15
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 15
LENGTH: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 50.5%;
Best Local Similarity 97.4%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                               Matches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fuchs, Renate APPLICANT: Motz, Manfred
                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSITION IN GENOME:
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 77
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                                                                   IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELTSPVVAESPKKP 210
 IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
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                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                          for Windows Version 4.0
                                                                                                                                                            50.2%;
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N/A
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Pred. No. 2.8e-60;
3; Mismatches 2
                                                                                                                                         Score 933; DB 4;
Pred. No. 6.4e-60;
3; Mismatches 1
                                                                                                                                             1; Indels
                                                                                                                                                                             Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 210
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                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MATGARET C.
REGISTRATION NUMBER: 25,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrella Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 29-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Upton
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: BNL93-28A
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                            Local Similarity
                                            KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                             IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
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 ELTSPVVAESPKKP 194
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                               IGKKIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN
                                                                                                                                                                                                                             188;
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o. 6248562
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                                                                                                                                                                                                                          Score 932; DB 4;
Pred. No. 7.6e-60;
3; Mismatches 3
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                                                                                                                                                                                                                                                         Length 210,
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197

ELTSPVVAESPKKP 210

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RESULT 7
US-08-235-836C-107
; Sequence 107, Application US/08235836C
; Patent No. 6248562
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                                                                                                                                                                                                                                                                                                                                                          uery Match
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein 08-235-836C-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
CROSSIFICATION DATA:
APPLICATION NUMBER: US
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                                                                                                      406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rela
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                             466
                                                                                                         184 SPVVAESPKKPSMVNNSGKDGNTSANSADESVK 216
                                                                                                                                                                                 124
                                                                                                                                                                                                       346 KIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 405
                                                                                                                                                                                                                                                              TITLE OF INVENTION: No. 6248562el Chimeric Proteins
TITLE OF INVENTION: Borrelia Polypeptides and Uses 7
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APPLICANT: Luft, Benjamin
                                                                                                                                                                                                                        64 KIHONNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETETNKLK 123
                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/01
FILING DATE: 29-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                             EKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT 183
                                                                                        SPVVAESPKKPGTMAQYNQMHMLSNKSASQNVR 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version
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                                                                                                                                                                                                                                                                                                                                      Score 929; DB 4; Length 588; Pred. No. 4.7e-59;
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US-08-158-353-2

; Sequence 2, Application US/08158353
; Patent No. 5620862
; GENERAL INFORMATION:
; APPLICANT: Padula, Steven J.
; TITLE OF INVENTION: Methods for D
TITLE OF INVENTION: Disease
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08,
FILING DATE: 29-APR-1994.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
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 CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton,
                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: BN TELECOMMUNICATION INFORMATION:
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APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                    184 SPVVAESPKKP 194
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                                                                                                                                                                                                                                                 456 SPVVAESPKKP 466
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TELEPHONE: (516) 282-3729
TELEPHONE: (516) 282-3729
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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STATE: NY
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amino acid
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   Brook,
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Smith & Reynolds,
                                                                        Diagnosing Early Lyme
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STREET: CITY: L

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; MOLECULE TYPE:
US-08-158-353-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                  APPLICANT: LIVEY, Ian
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND COMPOSITION FOR
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
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                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                               178 SVKELTSPVVAESPKKP 194
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196 SVKELTSPVVAENPKKP 212
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                                                                                           COUNTRY:
                                                                                                         CITY: Washington, D.C.
                                                                                                                         STREET:
                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                              ZIP: 20007-5109
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                                                                                                                       E: Foley & Lardner 3000 K Street, N.W.,
                                                                                           USA
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Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 685; DB 1; Length 212; Pred. No. 3.8e-42;
                                                                                                                         Suite 500
Version
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US-07-903-580-2
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                                                                                                                                                                                                                                                                                                                              Sequence 2, Applic
Patent No. 6221363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LIVEY, Ian
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AI
TITLE OF INVENTION: PREVENTION
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/824,161 FILING DATE: 22-JAN-1992 PRIOR APPLICATION DATA:
                 COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 VKELTSPVVAESPKKP 194
                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 199303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEG-LKEKIDAAKKCSETF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                         COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/727,245 FILING DATE: 11-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MACNNSGKDGNT-SANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS
                                                                                                                                                                                                                                                                                                                                                                                                                                          VKELTSPVVAETPKKP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMINO ACID
                                                                                                                                                                                                                                                                                                                                               Application US/07903580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
PatentIn Release #1.0,
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                                                                                                                                                                                                                                     METHOD AND COMPOSITION FOR THE PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.0%;
73.0%;
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Pred. No. 4.5e-41;
5; Mismatches 36
Version #1.25
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US-08-158-353-4
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Patent No. 5620862
GENERAL INFORMATION:
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                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                 APPLICANT: Padula, Steven J.
TITLE OF INVENTION: Methods for Diagnosing Early Lyme
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                               STREET: Two ...
CLASSIFICATION: 435
                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                    COUNTRY: U:
ZIP: 02173
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                                                                                                                                                                                                                                                                                                                                                                                          197 VKELTSPVVAETPKKP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                    137 TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                             ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 TNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
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LENGTH: 212 amino acids
TYPE: AMINO ACID
TOBOLOGY INO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
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NAME: BENT, Stephen A.
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PRIOR APPLICATION DATA:
US 07/727,245
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APPLICATION NUMBER: US 07/824,161
FILING DATE: 22-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEG-LKEKIDAAKKCSETF 118
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                         US/08/158,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.0%; Score 670; DB 4; 73.0%; Pred. No. 4.5e-41;
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APPLICANT: Wotz, Manfred
APPLICANT: Wotz, Manfred
APPLICANT: Wolse, Bettina
APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
ITILE OF INVENTION: Active proteins from Borrelia
FILE REFERENCE: 738.001US2
CURRENT APPLICATION NUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER FILING DATE: 1999-06-19
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-22
EARLIER FILING DATE: 1990-12-22
EARLIER APPLICATION NUMBER: WD PCT/EP90/02282
EARLIER FILING DATE: 1990-12-22
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER FILING DATE: 1990-06-13
NUMBER OF SEO ID NOS: 16
; ORGANISM: Borrelia burgdorferi
US-09-196-293-11
                                        NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 212
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US-09-196-293-11
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Patent No. 6183755
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 VKELTSPVVAESPKKP 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 TNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Carroll, Alice O. REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 ATGOKIDNNNGLAALNNONGSLLAGAYAISTLITEKLSKLKNLEELKTETAKAKKCSEEF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 ISĆNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MACNNSGKDGNT-SANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 212 amino acids
amino acid
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
                                                                                                                                                       TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/EE
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SOUTSCHECK, ERWIN
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS
TITLE OF INVENTION: FROM BORRELIA BURGDORFERI
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ent No.
ANTI - DENOL: N/A
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
----NISM: B. BURGDORFERI
                                                      DESCRIPTION: PROHYPOTHETICAL: N/A
ANTI-SENSE: N/A
                                                                                                                                                                                                      TELEPHONE: (212) 697-3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FUCHS, RENATE APPLICANT: WILSKE, BETTI
                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
CITY: N
STATE:
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                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/209,603E FILING DATE: 10-MAR-1994 CLASSIFICATION: 436
                                                                                                                                                                                                                                  NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9217-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
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TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNKLKEKHTDLGKEGYTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIGKKIHONNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKN-EGLKEKIDAAKKCSETF 118
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10016
R PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08209603E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WILSKE, BETTINA
PREAC-MURSIC, VERA
MOTZ, MANFRED
                                                                                      PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              MS-DOS Version 6.2
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                                                                                                                                                                                                                                                                                                           US 07/862,535
                                                                                                                                                                                                                                                                                                                                        PCT/EP90/02282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.8e-38;
3; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
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US-08-235-836C-34
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; ORIGINAL SOURCE:
US-08-209-603E-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                         TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
ANTI-SENSE: N/A
                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: DSM 566
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
ZIP: 11973
                                                                                   TELEPHONE:
                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                   Upton
                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                     (516)
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PATENT NO. 62400000
PATENT INFORMATION:
APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
APPLICANT: LUTT, BENJAMIN J.
APPLICANT.
APPL
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0
FILING DATE: 01-11-93
ATTORNEY_AGENT INFORMATION:
                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 VKELTSPVVAESPKKP 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 TNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                          NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324 REFERENCE/DOCKET NUMBER: BN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 29-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Brookhaven National Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08235836C
212 amino acids
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                                                                                                                                                          282-3729
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                                                                                                                                                                                                                                                                                                                     BNL93-28A
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Pred. No. 3.8e-38;
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; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-235-836C-34

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US-08-235-836C-32
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US-08-235-836C-32
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Best Local Similarity
                                                                                                                                               TELEPHONE: (516) 282-7338
TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
                         Query Match
                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BLD3-28A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32, Application US/08235836C Patent No. 6248562 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.7
Best Local Similarity 69.4
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 119/3
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/235,836C
                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 VKELTSPVVAESPKKP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 11973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 VKELTSPVVAESPKKP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Upton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 TNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 AIGKKIHONNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETF 118
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                                                                                                                                                                                   6) 202
) 282-3729
NO: 32:
   33.1%;
68.2%;
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Score 614.5; DB 4; Pred. No. 4.1e-37;
               Length 209;
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195 KELTNPVVAESPKKP 209
                 180 KELTSPVVAESPKKP 194
                                             135 NRLKGSHAQLGVAAATDDHAKEAILKSNPTKDKGAKALKDLSESVESLAKAAQEALANSV 194
                                                             120 NKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSV 179
                                                                                                                61 IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKN-EGLKEKIDAAKKCSETET 119
                                                                                                  75 IGKVIHQNNGLNANAGQNGSLLAGAYAISTLITEKLSKLKNSEELNKKIEEAKNHSEAFT 134
                                                                                                                                                      17 ISCNNSG--GDTASTNPDESAKGPNLTVISKKITDSNAFVLAVKEVEALISSIDELANKA 74
                                                                                                                                                                     Conservative
                                                                                                                                                                                                               20;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                              39;
                                                                                                                                                                                                            Indels
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2;

Search completed: March 18, 2002, 09:55:32 Job time: 345 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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length: 2000000000
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3148936 seqs, 277657034 residues
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1859
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            / cyn2_6/ptodata/2/paa/US085_COMB.pep: *
/cgn2_6/ptodata/2/paa/US085_COMB.pep: *
/cgn2_6/ptodata/2/paa/US086_COMB.pep: *
/cgn2_6/ptodata/2/paa/US087_COMB.pep: *
/cgn2_6/ptodata/2/paa/US088_COMB.pep: *
/cgn2_6/ptodata/2/paa/US089_COMB.pep: *
/cgn2_6/ptodata/2/paa/US099_COMB.pep: *
/cgn2_6/ptodata/2/paa/US092_COMB.pep: *
/cgn2_6/ptodata/2/paa/US092_COMB.pep: *
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/cgn2_6/ptodata/2/paa/US096_COMB.pep: *
/cgn2_6/ptodata/2/paa/US096_COMB.pep: *
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/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
/cgn2_6/ptodata/2/paa/US081_COMB.pep:*
/cgn2_6/ptodata/2/paa/US082_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

						Result	
98	76	4 0	· w	Ν	_		
1802.5	1805.5	1834 1810.5	1834	1859	1859	Score	
97.0 86.8	97.1 97.0	98.7 97.4	98.7	100.0	100.0	124	æ
	374 398					Length DB	
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US-09-596-746A-60	US-09-596-746-24 US-09-596-746-60	US-09-596-746A-80 US-09-596-746A-24	US-09-596-746-80	US-09-596-746A-28	US-09-596-746-28	ID	
Sequence Sequence		Sequence Sequence			Sequence	Description	
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App	App	App	App	App	App	! ! !	

14.5 86.8 377 19 US-09-596-746A-89.5 85.5 401 19 US-09-596-746A-1556 84.2 374 19 US-09-596-746A-1556 84.2 379 19 US-09-596-746A-1558 83.8 397 19 US-09-596-746A-31.558 82.2 370 19 US-09-596-746A-32.5 82.2 370 19 US-09-596-746A-32.5 82.2 370 19 US-09-596-746A-32.5 82.1 395 19 US-09-596-746A-32.5 80.3 384 19 US-09-596-746A-32.5 80.3 385 19 US-09-596-746A-32.5 80.3 408 19 US-09-596-746A-32.5 80.3 408 19 US-09-596-746A-32.5 80.3 409 19 US-09-596-746A-32.5 80.3 30.3 409 19 US-09-596-746A-32.5 80.3 30.3 19 US-09-596-746A-32.5 80.3 30.3 19 US-09-596-746A-32.5 80.3 370 19 US-0	14.5 86.8 377 19 US-09-596-746A-30 Sequence 89.5 85.5 401 19 US-09-596-746A-82 Sequence 89.5 85.5 401 19 US-09-596-746A-26 Sequence 1568 84.2 374 19 US-09-596-746A-26 Sequence 1558 83.8 397 19 US-09-596-746A-26 Sequence 1558 83.8 397 19 US-09-596-746A-64 Sequence 25.5 82.2 370 19 US-09-596-746A-64 Sequence 25.5 82.1 394 19 US-09-596-746A-64 Sequence 25.5 80.8 385 19 US-09-596-746A-40 Sequence 25.5 80.8 385 19 US-09-596-746A-40 Sequence 29.5 80.4 369 19 US-09-596-746A-76 Sequence 29.5 80.1 368 19 US-09-596-746A-76 Sequence 29.5 80.1 368 19 US-09-596-746A-78 Sequence 29.5 80.1 368 19 US-09-596-746A-78 Sequence 29.5 80.1 368 19 US-09-596-746A-78 Sequence 29.5 80.0 39.2 19 US-09-596-746A-72 Sequence 29.5 80.0 39.3 19 US-09-596-746A-72 Sequence 29.5 80.0 39.3 19 US-09-596-746A-72 Sequence 29.5 80.0 39.3 19 US-09-596-746A-74 Sequence 29.5 80.0 39.3 19 US-09-596-746A-72 Sequence 20.5 80.0 39.3 19 US-09-596-746A-74 Sequence 20.5 80.0 39.3 19 US-09-596-746A-74 Sequence 20.5 80.0 39.4 19 US-09-596-746A-74 Sequence 20.5 80.6 80.9 39.4 19 US-09-596-746A-74 Sequence 20.5 80.0 30.8 19 US-09-596-746A-74 Sequence 20.5 80.0 30.9 19 US-09-596-746A-74 Seque	л	44	4 3	42	41	40	39	38	37	36	<u>ა</u>	34 4	ω w	32																16	15	14	13			
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-09-596-746A-8 -09-596-746A-8 -09-596-746A-8 -09-596-746A-3 -09-596-746A-3 -09-596-746A-3 -09-596-746A-3 -09-596-746A-8 -09-596-746A-8 -09-596-746A-8 -09-596-746A-7	-09-596-746A-30 Sequenc -09-596-746A-82 Sequenc -09-596-746A-82 Sequenc -09-596-746-62 Sequenc -09-596-746-63 Sequenc -09-596-746-64 Sequenc -09-596-746A-64 Sequenc -09-596-746A-67 Sequenc -09-596-746A-78 Sequenc -09-596-746A-78 Sequenc -09-596-746A-78 Sequenc -09-596-746A-78 Sequenc -09-596-746A-72 Sequenc -09-596-746A-52 Sequenc -09-596-746A-65 Sequenc -09-596-746A-65 Sequenc -09-596-746A-65 Sequenc -09-596-746A-65 Sequenc -09-596-746A-65 Sequenc -09-596-746A-65 Sequenc -09-596-746A-65 Sequenc -09-596-746A-65 Sequenc -09-596-746A-65 Sequenc -09-596-746A-68 Sequenc -09-596-746A-54 Sequenc -09-596-746A-54 Sequenc -09-596-746A-68 Sequenc -09-596-746A-69 Sequenc -09-596-746A-69 Sequenc	19	9	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19
	sequence	S-09-596-746-70	-09-596-746A-6	-09-596-746-6	-09-596-746-3	-09-596-746A-5	-09-596-746-5	-09-596-746A-3	-09-596-746A-7	-09-596-746-7	-09-596-746-4	-09-596-746A-4	-09-596-746A-6	-09-596-746-6	-09-596-746-3	-09-596-746A-3	-09-596-746A-5	-09-596-746-5	-09-596-746A-7	-09-596-746-7	-09-596-746-40	-09-596-746A-7	-09-596-746-7	-09-596-746A-4	-09-596-746-56	-09-596-746A-5	-09-596-746A-6	-09-596-746-6	-09-596-746-3	-09-596-746A-3	-09-596-746A-6	-09-596-746-6	-09-596-746-2	S-09-596-746A-2	S-09-596-746A-8	S-09-596-746-8	IS-09-596-746A-3
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ALIGNMENTS

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RESULT 1
US-09-596-746-28
; Sequence 28, Application US/09596746
; GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Maria J.C. Gomes Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 50/140,042
SOFTWARE: FEASTSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 378
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OSPEC Chimera
US-09-596-746-28
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Query Match 100.0%; Score 1859; DB 19; Length 378; Best Local Similarity 100.0%; Pred. No. 4.5e-123; Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: OSPC Chimera
                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Score 1859; DB 19;
Matches 378; Conservative 0; Mismatches 0;
        181 ELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEV 240
                                            121 KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                          121 KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGABELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                                                                                                                                             CURRENT PAPILCATION NUMBER: US/09/596,746A
PRIOR APPLICATION NUMBER: US/09/596,746A
PRIOR APPLICATION NUMBER: US 60/140,042
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                         61 IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETETN 120
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FA
O ID NO 28
LENGTH: 378
TYPE: PRT
                                                                                                      61 IGKKIHQNNGLDTENNHNGSSLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETN 120
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Dykhuizen, Danial
APPLICANT: Maria Jenjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
FILE REFERENCE: 2631,1002-001
FILE REFERENCE: 2631,1002-001
FILE REFERENCE: 2631,1002-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Б
                                                                                                                                       1 MACNNSGKDGNTSANSADESVKGDNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL
                                                                                                                                                   1 MACNUSGRDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iequence 28, Appringer 1 NFORMATION:
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241 ETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IGKKIHONNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTN 120
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APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: Groups of Borrelia burgdorferi and COURENT APPLICATION. Borrelia afzelii That Cause Lyme Disease in Humans CURRENT APPLICATION NUMBER: US/09/596,746
PRIOR APPLICATION NUMBER: US/09/596,746
PRIOR APPLICATION NUMBER: US/09/596,746
NUMBER OF SEQ ID NOS: 199-06-18
SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: OSPC Chimera
385 SKAAKEMLTNSVKELTS 401
              362 SKAAKEMLTNSVKELTS 378
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Fast SEQ ID NO 80 LENGTH: 401
                 325 IEKAKKCSEEFTAKLKGEHTDIGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNL 384
                                302 IEKAKKCSEEFTAKLKGEHTDLGKEGYTDDNAKKAILKTNNDKTKGADELEKLFESYKNL 361
                                                              265 TLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAE 324
                                                                             242 TLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAE 301
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US-09-596-746-80
Connence 80, Ap
                                                                                                          205 LTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVE 264
                                                                                                                        182 LTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVE 241
                                                                                                                                                         145 LKEKHTDLGKEGVTDADAKEAILKTNGTKTKGABELGKLFESVEVLSKAAKEMLANSVKE 204
                                                                                                                                                                       122 LKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLEESVEVLSKAAKEMLANSVKE 181
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                                                                                                                                                                                                                                                                                                                          Similarity 98.9
173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dattwyler, Raymond J.
Seinost, Gerald
                                                                                                                                                                                                                                                                                                   98.7%; Score 1834; DB 19; Length 401; 11ve 2; Mismatches 2; Indels 0;
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Sequence 24, Application US/09596746A
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in I
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
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SEQ ID NO 80
LENGTH: 402
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
FILE REFERENCE: 2631.1002-001
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
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GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 98.7
Best Local Similarity 98.9
Matches 373; Conservative
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ORGANISM: OSPC Chimera
9-596-746A-80
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Pred. No. 2.9e-121;
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Sequence 24, Application US/09596746

GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Deinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
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; OTHER INFORMATION: OSPC Chimera
US-09-596-746A-24
; OTHER INFORMATION: OSpC Chimera US-09-596-746-24
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NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 24
LENGTH: 375
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Best Local Similarity
                                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial
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98.1%;
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Pred. No. 1.2e-119;
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Lyme Disease
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Query Match

97.18;

Score 1805.5;

DB 19;

Length 374;

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APPLICANT: Dattwier, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
RIOR APPLICATION NUMBER: US/09/596,746
RIOR APPLICATION NUMBER: US 60/140,042
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 398
                                                                                                                                                                                                                                                                                         ; ORGANISM: OSPC Chimera
US-09-596-746-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-596-746-60
                                                                                                                                                                                                                    Matches 369;
                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 60, Application US/09596746 GENERAL INFORMATION:
                       2 ACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDBIAAKAI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 SKAAKEMLTNSVKELTS 378
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                                                                                                                                          SCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI 84
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hes 370; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKAAKEMLTNSVKELTS 374
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2; Mismatches 2;
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LENGTH: 399
TYPE: PRT
ORGANISM: OSPC Chimera
US-09-596-746A-60
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US-09-596-746A-60
; Sequence 60, Application US/09596746A
; GENERAL INFORMATION:
; APPLICANT: Dattwyler, Raymond J.
; APPLICANT: Seinost, Gerald
; APPLICANT: Luft, Benjamin J.
; APPLICANT: Luft, Benjamin J.
; APPLICANT: Maria J.C. Gomes-Solecki
; TITLE OF INVENTION: Groups of Borrelia burgdorferi and
; TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
; FILE REFERENCE: 2631.1002-001
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383 SKAAKEMLTNSVKELTS
                                                                                                                   242 TLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAE
                                                                                                                                                                           182 LTSPVVAESPKKPSMYNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVE 241
                                                                                                                                                             206 LTSPVVAES---PAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVE
                                                                                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                          62 GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK 121
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               SKAAKEMLTNSVKELTS 378
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                                                           IEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNL
                                                                                                   TLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAE
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369; Conserv
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97.9%;
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Pred. No. 4.8e-119;
3; Mismatches 2; Indels 3;
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3; Gaps

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US-09-596-746-30

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US-09-596-746A-30
(Sequence 30, Application US/09596746A
(Sequence 30, Application US/09596746A
(GENERAL INFORMATION:
(APPLICANT: Dattwyler, Raymond J.
(APPLICANT: Seinost, Gerald
(APPLICANT: Seinost, Gerald
(APPLICANT: Luft, Benjamin J.
(APPLICANT: Matia J.C. Gomes-Solecki
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GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Scinost, Gerald
APPLICANT: Dykhuizen, Danial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 331; Conserva
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SEQ ID NO 30
SEQ ID NO 30
STYPE: PRT
ORGANISM: Artificial Sequence
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CURRENT APPLICATION NUMBER: US/09/596,746

CURRENT FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR FILING DATE: 1999-06-18

NUMBER OF SEO ID NOS: 84

CONTRADED: TESTETS: 84
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APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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87.8%; Pred. No. 9e-106;
tive 20; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377
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                                                            Disease
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                                                         Humans
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APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Dises
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 82
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CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 377
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; OTHER INFORMATION: OSPC Chimera
US-09-596-746A-30
US-09-596-746-82
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                                                                                                                                                                                                                                                                                                                                     Sequence 82,
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APPLICANT:
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TYPE: PRT
ORGANISM: Artificial Sequence
                                 LENGTH: 4
TYPE: PRT
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Pred. No. 9e-106
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TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in FILE REFERENCE: 2631.1002-001

VORRENT APPLICATION NUMBER: US/09/596,746A

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR EILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 4.0

TYPE: PRT

TYPE: PRT
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US-09-596-746A-82
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Best Local
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Best Local (
                                      Local Similarity
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Seinost, Gerald
                                                                                                                                                            Conservative
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                                                                                                                                                      85.5%; Score 1589.5; DB 19
86.7%; Pred: No. 5.8e-104;
Mismatches 27;
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86.7%; Pred. No. 5.7e-104;
tive 22; Mismatches 27; Indels
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; OTHER INFORMATION: OSPC Chimera
US-09-596-746A-26
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US-09-596-746A-26
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LENGTH: 374

TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 85.9%; Pred. No. 2.
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
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              300 AEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVK
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ETLLASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLK
                                                                              ETLLTSIDELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELK
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nes 27;
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374 376

US-09-596-746-26

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Sequence 26, Application US/09596746
(GERERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in I
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
NUMBER OF SEQ ID NOS: 84
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                                                                     RESULT 15
US-09-596-746-62
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SEQ ID NO 26
LENGTH: 373
                                        Sequence 62, Application US/09596746 GENERAL INFORMATION:
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Best Local Similarity
Matches 323; Conserv
APPLICANT:
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APPLICANT:
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ORGANISM: Artificial Sequence
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LAKAAKEMLANSVKEL 373
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                                                                                                                                                    LSKAAKEMLTNSVKEL 376
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Dykhuizen, Danial
             Dattwyler, Raymond J.
Seinost, Gerald
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85.9%; Pred. No. 5.46
tive 22; Mismatches
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Search completed: Job time: 971 sec

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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 62
LENGTH: 397
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                     Matches 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT APPLICATION NUMBER: US/09/596,746
PRIOR APPLICATION NUMBER: US/09/596,746
PRIOR APPLICATION NUMBER: US/09/596,746
PRIOR FILING DATE: 1999-06-18
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                                                                301 EIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKN
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85.6%; Pred. No. 9.6e-102;
tive 23; Mismatches 27;
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

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US-09-748-875-63
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US-09-614-150-6213	US-09-561-709B-7	US-09-961-403-7	US-09-614-150-4824	US-09-614-150-10311	US-09-614-150-10224	US-10-072-851-12610	US-09-815-242-12610	US-10-072-851-5639	US-09-815-242-5639	US-09-708-427-21159	US-09-708-427-21160	US-09-708-427-21161	US-09-748-875-60	US-09-748-875-2	US-09-748-875-62	US-09-748-875-1	US-09-748-875-61	US-09-748-875-14	US-09-708-427-15046
Sequence 6213, Ap	Sequence 7, Appli	Sequence 7, Appli	Sequence 4824, Ap	Sequence 10311, A	Sequence 10224, A	Sequence 12610, A	Sequence 12610, A	Sequence 5639, Ap	Sequence 5639, Ap	Sequence 21159, A	Sequence 21160, A		Sequence 60, Appl	Sequence 2, Appli	Sequence 62, Appl	Sequence 1, Appli	Sequence 61, Appl	Sequence 14, Appl	Sequence 15046, A

ALIGNMENTS

SEQ ID NO 5 LENGTH: 211 TYPE: PRT ORGANISM: Borrelia burgdorferi US-09-974-992-5 us-09-974-992-5 Sequence 5, Application US/09974992 GENERAL INFORMATION: APPLICANT: Mathiesen, Marianne J. APPLICANT: Theisen, Michael APPLICANT: Holm, Arne APPLICANT: Ostergaard, Soren TITLE OF INVENTION: Novel OspC-derived peptide fragments FILE REFERENCE: 459-666P CURRENT APPLICATION NUMBER: US/09/974,992 CURRENT FILING DATE: 2001-10-10 PRIOR APPLICATION NUMBER: 09/180,089 PRIOR FILING DATE: 1999-05-13 PRIOR APPLICATION NUMBER: PCT/DK97/00203 PRIOR FILING DATE: 1997-05-02 NUMBER OF SEQ ID NOS: 40

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RESULT 2 US-09-974-992-7

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; SEQ ID NO 3
; LENCTH: 207
; TYPE: PRT
; ORGANISM: Borrelia g
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TYPE: PRT
: ORGANISM: Borrelia afzelii
US-09-974-992-7
                    Query Match
Best Local Similarity
             Matches 128;
                                                                                                                                                                                                                               APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: NOVel OspC-derived peptide fragments
FILE REFERENCE: 459-666p
CURRENT APPLICATION NUMBER: US/09/974/992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
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PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
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CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mathiesen, Marianne J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
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|NERAL INFORMATION:
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al Similarity 69.9%;
137; Conservation
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      32.1%; So ilarity 66.0%; Pr Conservative 25;
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                    Score 596.5; DB (
Pred. No. 2.5e-33
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Best Local Similarity
Matches 100; Conserv
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APPLICANT: Terry, Roemer D.
APPLICANT: BO, Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1 SEQ ID NO 7646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Howard, Bussey TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery FILE REFERENCE: 10182-005-999 CURRENT APPLICATION NUMBER: US/10/032,585 CURRENT FILING DATE: 2001-12-20 NUMBER OF SEQ ID NOS: 8000
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             1746
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 ISCNNSG--GDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDEL-SKA
       LQFLSGNKSKELEDYIQK----
                                                                                                                                            TSIEE--KNNQIKELSETIKSLKTELKTSGDALKQSQKEYKTLKTKNSDTESKLEKQLEE
                                                                                                                                                                              NSADESVKGPNLTEISKKI-----TESNAVVLAVKEVETLLTSIDELAKAIGK----
                                                                      LEKVKSDLQTADE-KLKGITEREIALKSELETVKNSGLSTTSELAALTKTVKSLEKEKEE
                                                                                                      --KIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA-----EIEKAK-- 306
                                                                                                                                                                                                                                                     TKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVVAESPKKPSMVNNSGKDGNTSA 208
                                                                                                                                                                                                                                                                                                                               SETFTNKLKEKHTDLGKEGVTDADAKEAILKA----
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                                  -KCSEEFTAKLKGEHTDLGK--EGVTD------DNAKKAILKTNNDKTK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boone
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21.0%;
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-HSDISEKLKALTDELKEKTKQFDDSKKKLTELENDLTS 1801
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Pred. No. 0.0025;
'8; Mismatches 171;
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; LOCATION: (1881)..(1881)
; OTHER INFORMATION: X=any amino acid
US-10-072-851-15590
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Best Local s
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 15590
LENGTH: 1881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                1687 LEKVKSDLQTADE-KLKGITEREIALKSELETVKNSGLSTTSELAALTKTVKSLEKEKEE 1745
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   307
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                                                                                                                                                                                                                                                                                               LTK---SSKDLEVCGNQKSELQDSLKS----VKSELKNFENKYNQETTSLKDEIEEKQKE 1523
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                                                                                                 TSIEE--KNNQIKELSETIKSLKTELKTSGDALKQSQKEYKTLKTKNSDTESKLEKQLEE 1686
                                                                                                                            NSADESVKGPNLTEISKKI-----TESNAVVLAVKEVETLLTSIDELAKAIGK----
                                                                                                                                                               QKTSLKQDIAKLSQDHE-SAQTQLEDKENQLKEL------KASL----EKHNTESA 1628
                                                                                                                                                                                                                                                               SETETNKLKEKHTDLGKEGVTDADAKEAILKA-----
                                                               --KIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA-----EIEKAK--
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   -----KCSEEFTAKLKGEHTDLGK--EGVTD----
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Boone, Charles
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Yamamoto, Robert T.
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Zyskind, Judith W
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Zamudio, Carlos
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21.0%; Pred. No. 0.0025;
ative 78; Mismatches 171;
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Best Local Similarity
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TYPE: PRT
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: LOCATION: 1..1313
OTHER INFORMATION: Xaa is any amino acid
: NAME/KEY: misc_feature
: LOCATION: 1..1313
: OTHER INFORMATION: Ceres Seq. ID 1828627
US-09-708-427-15044
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APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 15044
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NAME/KEY: misc_feature
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KATLLYCQEELKNC---ESQVDSLKLASKETNEKYEKMLEDARNEIDS 486
                                                              KAILKTNNDKTKGADELEKLFESVKNLSKAAKE----MLTNSVKELTS 378
                                                                                                                                                                  ISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAK 334
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                                                                                                                               -----IQNLLDQRTELSIELERCKVEEEKSKKDMESLTLAL------QEASTESSEA 441
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21.8%;
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ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1.1304
OTHER INFORMATION: Xaa is any amino ac
NAME/KEY: misc_feature
LOCATION: 1.1304
COCATION: 1.1304
OTHER INFORMATION: Ceres Seq. ID 18286
US-09-708-427-15045
                RESULT 8
US-09-708-427-19883
; Sequence 19883, Application
; GENERAL INFORMATION:
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US-09-708-427-15045
; Sequence 15045, Application US/09708427
; Sequence 15045, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; FILE REFERENCE: 2750-1243P
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 15045
LENGTH. 1304
TYPE: PRT
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                                                                                                                                      LEKLFESVKNLSKAAKE----MLTNSVKELTS
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                                    US/09708427
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CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09
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US-09-708-427-19882

Sequence 19882, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                         RESULT
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 19883
LENGTH: 1014
TYPE: PRT
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
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OTHER INFORMATION: Xaa is
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; LOCATION: 1..1018
; OTHER INFORMATION: Xaa is i
; NAME/KEY: misc_feature
; LOCATION: 1..1018
; OTHER INFORMATION: Ceres S:
US-09-708-427-19882
                                                                        Sequence 1988) Application US/09708427
(GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRA
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243p
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 83564
SOFTWARE: Patentin version 3.1
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US-09-708-427-19881
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Matches 113; Conserv
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SOFTWARE: PatentIn version
SEQ ID NO 19882
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Best Local :
                                                            SEQ ID NO 19881
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ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
                      TYPE: PRT
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; LOCATION: 1..1269
; OTHER INFORMATION: Ceres
US-09-708-427-19881
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US-09-815-242-5883
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                                                                                              APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yyamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1269
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         656 KHGETEADSKGYLGQVAELQSTLEAFQVKSSSLEAALNIATENEKELTENLNAVTSEKKK 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 VLAVKEVETLLTSIDELA-KAIG------KKIKN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      716 LEA---TVDEYSVKISESENLLESIRNELNVTQG-KLESIENDLKAAGLQESEVMEKLKS 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 VEALLSSIDETAAK------AIGKKIHQNNGLDTENNHNGSLLAGAYAISTL--IKQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 KLDGLKNEGLKEKIDAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASVKVAELTS 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KQLTSEGEKLQSQIEKLRAVAAEKSVLESH - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TSPVVAESPKK-----PSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDLEGKIKSYEEQLAEASGKSSSLKEKLEQTLGRLAAAESVNEKLKQEFDQAQEKSLQSS 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEESLEQKG--REIDEATTKRMELEALHQSLSIDSEHRLQKAMEEFTSRDSEASSLTEKL 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDGNTSANSADE - - - - - - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SESELLAETNNQLKIKIQELEGLIGSGSVEKETALKRLEEAIE-----RFNQKETESSDL 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDL-GKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----DVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA-EIEKAKKCSEEFT 313
                                                                                                                                                                                                                                                                                                     Zyskind, Judith W. Wall, Daniel
                                                                                                                                                                                                                                                                                 Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 167.5; DB 6; Pred. No. 0.0027;
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 5883
                                                                                                                                                                                                                                                                                                              US-10-072-851-5883; Sequence 5883, Application; GENERAL INFORMATION:
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                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
            APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA 028A
                                                                                                                                                                                                                              APPLICANT:
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Best Local :
     CURRENT
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAKQALNGNANVQHAKDEATALINSSNDLNQAQKDALKQQVQNATT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKELTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KISAIKDSGELKAEI-----EKAKK-----CSEEFTAKLKGEHTDLG--KEGVTDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDAAKKCSETFTNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQS------LGSLDNLNNAQKQTVTDQINGAHTVDEANQIKQNAQNLNTAMGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKÄAKEMLANSVKELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQQSTTVAEAQGNEQKANNVDAAMDKLRQSIADNATTKQNQNYTDASQNKKDAYNNAVTT
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                                                                                                            Yamamoto, No.
                                                                                                                                                                                                                                                                                                 Carr, Grant J.
                                                                                   Jiang, Bo
Boone, Charles
                                                                                                                                                        Trawick, John D.
                                                                                                                                                                           Wall, Daniel
                                                                                                                                                                                          Ohlsen, Kari L.
Zyskind, Judith W
                                                                                                                                                                                                                                           Foulkes, J. Gordon
Zamudio, Carlos
                                                                                                                                                                                                                            Haselbeck, Robert
                                                                                                                                                                                                                                                                             Xu, H. Howard
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NUMBER: US/10/072,851
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18.7%;
                                                                                                                                         Robert T
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                                                    the
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                                                  Target
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                                                  Compound which
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                                                  Inhibits
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; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 5883
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-072-851-5883
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Best Local
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671 AAKQALNGNANVQHAKDEATALINSSNDLNQAQKDALKQQVQNATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53
                                                                                                                                                                                      LKQAIADKDATKATVNFTDADQAKQQAYNTAVTNAENIISKANGGNATQAEVEQAIKQVN 670
                                                                                                                                                                                                                                                                               KISAIKDSGELKAEI-----EKAKK------CSEEFTAKLKGEHTDLG--KEGVTDDN 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TESNAVVLAVKEVETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITK 287
                                                                                        AKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKELTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKAAKEMLANSVKELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKI 227
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18.7%;
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Pred. No. 0.0033;
Nicmatches 181;
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US-09-815-242-13080
                                                                    CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                   PRIOR
PRIOR
                                                                                                                                                                                                                      TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                   PRIOR
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               APPLICATION NUMBER: 60/253,625
                                   APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
FILING DATE:
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Yamamoto, Robert T.
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16

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US-10-072-851-13080
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Best Local Similarity
Watches 76; Conserve
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SOFTWARE: FBStSEQ for Windows Version 4.0
SEQ ID NO 13080
LENGTH: 875
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APPLICANT:
APPLICANT:
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NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                          APPLICANT: Bussey, Howard TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits TITLE OF INVENTION: Proliferation FILE REFERENCE: ELITER.028A CURRENT APPLICATION NUMBER: US/10/072,851 CURRENT FILING DATE: 2002-08-08
                                     PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
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Boone, Charles
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Yamamoto, Robert T.
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Zyskind, Judith W.
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Zamudio, Carlos
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; LENGTH: 875
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-072-851-13080
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Best Local
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708
                                          333 AKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKELTS 378
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                                                                                                                                   288 KISAIKDSGELKAEI-----EKAKK------CSEEFTAKLKGEHTDLG--KEGVTDDN 332
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AAKQALNGNANVQHAKDEATALINSSNDLNQAQKDALKQQVQNATT
                                                                                         LKQAIADKDATKATVNFTDADQAKQQAYNTAVTNAENIISKANGGNATQAEVEQAIKQVN
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US-09-815-242-5835 PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23 GENERAL INFORMATION Sequence 5835, PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308 CURRENT APPLICATION NUMBER: US/09/815, CURRENT FILING DATE: 2001-03-21 TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes APPLICANT: Haselbeck, Robert PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27 FILE REFERENCE: ELITRA.011A APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: NUMBER OF SEQ ID NOS: 14110 PRIOR FILING DATE: APPLICANT: APPLICANT: FastSEQ Carr, Grant J.
Yamamoto, Robert T. Wall, Daniel Xu, H. Howard Trawick, John D. Zyskind, Judith W. Application US/09815242 for Windows Version 2001-02-16 of Essential Genes 'n

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; TYPE: PRT
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                                                                                            2263 NLNTAMGNLKQAIADKDATKATVNFTDADQAKQQAYNTAVTNAENIISKANGGNATQAEV 2322
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                                               325 KEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKELTS 378
                                                                                                                                    280 LISNLITKKISAIKDSGELKAEI-----EKAKK-----CSEEFTAKLKGEHTDLG-- 324
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Search completed: March 18, 2002, 09:58:19 Job time: 377 sec

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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M5_STRPY
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SCA4_RICAY
SCH1_CHICK
WYSP_SCHJA
ZITP1_YEAST
WYSN_DROME
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RBP1_DROME
SCA4_RICAY
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RBP1_DROME
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Q10411 schizosacch
P08089 streptococc
P19401 streptococc
Q9aix9 rickettsia
Q00799 plasmodium
P24733 aeguipecten
       P025386
P025666
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P0224697
P02246979
P020798
P030339
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                                                                                                                                                                                                                              homo sapien
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7 streptococc
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7 borrelia bu
8 borrelia he
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   streptococc
rattus norv
loligo peal
                                                                                                               homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homo sapien
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R., Palmer N., Adams M.D., Gocayne J.D., Weidman	Kerlavage A.R., Quackenbush J., Salzberg :	Richardson D.	.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,	5943; Pu	STRAIN-ATCC 35210 / B31;	UENCE	[5]	rgdorreri sensu tato isotates from J	C gene sequence analy	se A.;	ď	STRAIN=ATCC 35210 / B31;	SEQUENCE FROM N.A.		American strain of Borrelia burgdorieri."; Infect. Immun. 61:5097-5105(1993).	and exp	ieri A., Dias F., Szczepanski A., Ryan R.W.;	11630; Pu	SEQUENCE FROM N.A.		ect. Immun. 61:2182-2191(1993).	rgdorferi.	"Immunological and molecular polymorphisms of OspC, an immunodominant	E., Wanner G.;		MEDLINE=93239332; PubMed=8478108;			. Microbiol. Immunol. 182:37-50(1993).	ein C (OspC) and the flagellin of Borrelia burgdorferi.	etic heterogenity of the genes coding for the outer		Jauris-Heipke S., Fuchs R., Motz M., Preac-Mursic V., Schwab E.,	/ B31;			NCBI TRAXID=139:	Spirochaetales:	Borrelia burgdorferi (Lyme disease spirochete).	BB19.	CE PROTEIN C PRECURSOR (PC)	(Rel. 40,	1998 (Rel. 37, Created)		OSC1_BORBU STANDARD; PRT; 210 AA.	Ľ

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Hansen and taxonomy

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RESULT 2
OSC2_BORD
ID OSC2_B
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Best Local S
Matches 190
                                                                                                                                                                                                           OSC2_BORBU
Q08137;
                      MEDLINE-92219995; PubMed=1560779;
                                                                                               Borrelia burgdorferi (Lyme Bacteria; Spirochaetales;
                                           STRAIN-PKO;
                                                      SEQUENCE FROM N.A.,
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15-DEC-1998 (Rel. 37, Last announce
OUTER SURFACE PROTEIN C PRECUR
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X69596; CAA49306.1; -. EMBL; U01894; AAA16058.1; -. EMBL; D49497; BAA08457.1; -. EMBL; AE000792; AAC66329.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Nature 390:580-586(1997).

-!- FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.

-!- FUNCTION: NOT KNOWN; ATTACHED TO THE OUTER MEMBRANE
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Garland S., Fujii (
Smith H.O., Venter
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een the Swiss Institute of Bioinformatics and the EN
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210 AA;
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97.9%;
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3; Mismatches
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Pred. No. 2
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OUTER SURFACE PROTEIN C.
N-ACYL DIGLYCERIDE (BY SIMILARITY).
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       F.,
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                                                                                                            spirochete)
      Preac-Mursic
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                                                                                                                                                                                                                      212 AA
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EMBL outstation -
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R EMBL; X73624; CAA52003.1; -.

R InterPro; IPR001800; Lipoprotein_6: 1.

R Pfam; PF01441; Lipoprotein_6; 1.

R ProDom; PD001149; Lipoprotein_6; 1.

R ProDom; PD001149; Lipoprotein; Signal; Plasmid; Antigen.

M Outer membrane; Lipoprotein; Signal; Plasmid; Antigen.

T SIGNAL 1 B BY SINTEACE PROTEIN C.

T CHAIN 19 212 OUTER SURFACE PROTEIN C.

T LIPID 19 19 N-ACYL DIGLYCERIDE (BY SIMI)

SEQUENCE 212 AA; 22499 MW; C206C231FBF2E7D4 CRC64;
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Best Local :
                                                                                         01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
VARIABLE MAJOR OUTER MEMBRANE LIPOPROTEIN 24
                                                                                                                                                               VM24_BORHE
P32778;
                                                                                       VMP24
SEQUENCE FROM
                           NCBI_TaxID=140;
                                         Bacteria; Spirochaetales;
                                                         Plasmid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Theisen M., Frederiksen B., Lebech A.M., Vuust J., Hansen "Polymorphism in ospC gene of Borrelia burgdorferi and immunoreactivity of OspC protein: implications for taxono use of OspC protein as a diagnostic antigen."; J. Clin. Microbiol. 31:2570-2576(1993).

-!- EUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE
                                                                                                                                                                                                                                                                       179 VKELTSPVVAESPKKP 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular analysis and expression of a Borrelia burgdorferi gene encoding a 22 kDa protein (pC) in Escherichia coli."; encoli. microbiol. 6:503-509(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94075528; PubMed=8253951;
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                                                                                                                                                                                                                                                                                                            TIKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS
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                                                                                                                                                                                                                                                                                                                                                                                      AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETF 118
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                                       Spirochaetaceae;
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(BY SIMILARITY). CRC64;

Length Indels

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Gaps

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В Ş Дb Q DR FT FT FT FT

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Best Local S
Matches 91
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Interpro; IPR001800; L1por-
pfam; PF01441; L1poprotein_6; 1.
proDom; PD001149; L1poprotein_6; 1.
proDom; PS00013; PR0KAR_LIPPOPROTEIN; 1.
proprint; Signal; Plasmid.
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                                                                                                                                                                                                                                           BORHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are highly polymorphic.";
Mol. Microbiol. 6:3299-3311(1992).
             STRAIN-SSP. HS1 SEROTYPE 3;
MEDLINE-93133110; PubMed-1484486;
Restrepo B.I., Kitten T., Carter
                                          SEQUENCE FROM N.A. STRAIN-SSP. HS1 SE
                                                                                Bacteria; Spirochaetales;
NCBI_TaxID=140;
                                                                                                                                                      Ol-JUL-1993 (Rel. 26, Created)
Ol-JUL-1993 (Rel. 26, Last sequence update)
Ol-FEB-1994 (Rel. 28, Last annotation update)
VARIABLE MAJOR OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR
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"Subtelomeric expression regions of Borrelia hermsii linear plasmids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SSP. HS1 SEROTYPE MEDLINE-93133110; PubMed-
                                                                                                                 Plasmid
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 Subtelomeric expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSCNNGGPE-----LKSDEVAKSDGTVLDLAKVSKKIKEASAFAASVKEVETLVKSVDEL
                                                                                                                                                                                                                                                                                                  AEGEVEAAIKELTAPVKAEKPSQ
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214 /
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                                          SEROTYPE
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22541 MW;
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                                                                                                 Spirochaetaceae;
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No. 6.
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                Infante D., Barbour A.G.;
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01-NOV-1988 (Rel. 09, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
MYOSIN II HEAVY CHAIN, NON MUSCLE.
Acanthamoeba castellanii (Amoeba).
Eukaryota: Acanthamoebidae; Acanthamoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                          Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.;
"Complete nucleotide sequence and deduced polypeptide
nonmuscle myosin heavy chain gene from Acanthamoeba:
hinge in the rodlike tail.";
J. Cell Biol. 105:913-925(1987).
J. FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACT
ACTIVITY THAT IS ACTIVATED BY F-ACTIN.
-I- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT
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pfam; pF01441; Lipoprotein_6; 1.
proDom; pD001149; Lipoprotein_6; 1.
pROSITE; pS00013; pROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Plasmid.
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Mol. Microbiol. 6:3299-3311(1992).
-i- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE
FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
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InterPro; IPRO01609; myosin_head.
Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
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TODOM; PD00015; IQ; 1.

SMART; SM00015; IQ; 1.

SMART; SM00242; MYSS; 1.

PROSITE; PS50096; IQ; 1.

MYOSIN; Coiled coil; Actin-binding; ATP-binding; Calmosin; Coiled coil; Actin-binding; MIDSIN HEAD-LIKE.

MYOSIN HEAD-LIKE.
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                                                                                                                     YEDEAAAHDSLKKKEEDLSRE-LRETKDALADAENISETLRSKL--KNTERGADDVRNEL 104
                                                                                                                                                LAGAYAISTLIKQKLDGLKNEGLKEKIDA---AKKCSETFTNKLKEKHTDLGKEGVTDA- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NONHELICAL TAILPIECE WHERE THE REGULATORY PHOSPHORYLATION SITES RESIDE.
MISCELLANGEDUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTIVITY. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 2 1Q DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MLC-2).
DOMAIN: THE
CYCLES OF A
                                                                                                                                                                                                          EINKKITDSNAVLLAVKEVEA----LLSSIDEIAAKAIGKKIHQ--NNGLDTENNHNGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                       1489
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766
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1509
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1509
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                                                                                                                                                                                                                                                69;
                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                            Score 179; DB 1; pred. No. 0.33; 9; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                    METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
PHOSPHORYLATION.
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQ.
COILED COIL (POTENTIAL).
ALPHA-HELICAL TAILPIECE
                                                                                                                                                                                                                                                                                                                                                                                                               ACTIN-BINDING. ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALPHA-HELICAL TAILPIECE (LMM).
NONHELICAL TAILPIECE.
                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIGHT MEROMYOSIN (LMM)
                                                                                                                                                                                                                                                                                                                     2CE49BE51173D17E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions on ong as its content is in no
                                                                                                                                                                                                                                                                        Length 1509;
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                                                                                                                                                                                                                                            Indels
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          637
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z70690; CAA94624.1; -. Hypothetical protein. SEQUENCE 1957 AA; 222785
                                        232
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Q104011;
Q10-0CT-1996 (Rel. 34, Created)
Q1-0CT-1996 (Rel. 34, Last sequence update)
Q1-0CT-1996 (Rel. 34, Last sequence update)
Q1-0CT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 222.8 KDA PROTEIN C1F3.06C IN CHROMOSOME SPACIF3.06C.
                                                                                                                   534 LNELKGELQTEISNSEHLSSQLSTLAAEKEAAVATN-----NELSESKNSLQTLCNAF
                                                                                                                                                          127
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                                                                                                                                                                                                                                               419
                                                                                                                                                                                                                                                                                               360 KDSRTSNSQLEEEMVELKESNRT-IHSQLTDAESKLSSFEQENKSLKGSIDEYQNNLSSK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V., Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomyo
Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHPO
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SKLQQLQLERANFEQKESTLSDENNDLRTKLLKLEESNKSLIKKQEDVDSLE---
                                     AVVLAVK-----
                                                         QEKLAKSVMQL-----KENEQNFSSLDTSFKKLNESHQELEN-----NHQTITKQLKDTS
                                                                                     KEMLANSVKELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESN
                                                                                                                                                                                                                                     DKMVKQVSSQLEEARSSLAHATGKLAEINSERDFQNKKIKDFEKIEQDLRACLNSSSNEL
                                                                                                                                                                                                                                                                                                                           KDGNTSANSADE----SVKGPNLTEINKKITDSNAVLLAV-KEVEALLSSIDEI------
                                                                                                                                                                           KEK---SALIDKKDQELNN--LREQIKEQKKVSESTQSSLQSLQRDILNEKKKHEVYESQ
                                                                                                                                                                                                         AGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL-----KEKH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELLTAQEARAAAEK-NLDKAN--LELEELRQEADDAARDNDKLVKDNRK 1312
                                                                                                                                                                                                                                                                                                                                                                    108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVK
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                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                         --------AAKAIGKKIHQNNGLDTEN---
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                      -----TDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAA 171
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                                                                                                                                                                                                                                                                                                                                                                             9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     222785 MW;
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                                                                                                                                                                                                                                                                                                                                                            73;
                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                               Score 173.5;
Pred. No. 0.
                               EVETLLTSIDELAKAIGKKIKNDVSLDNEADHNGS
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                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  3F480CA06171D9DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ELKAEIEKAKK---CSEEFTAKLKGEHTDLGK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                              148;
                                                                                                                                                                                                                                                                                                                                                          Indels 145;
                                                                                                                                                                                                                                                                                                                                                                                        Length 1957;
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tent is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-86111835; PubMed-3511046;
Hollingshead S.K., Fischettl V.F., Scott J.R.;
"Complete nucleotide sequence of type 6 M protein of the
Streptococcus. Repetitive structure and membrane anchor."
J. Biol. Chem. 261:1677-1686(1986).
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                     Pfam; PF02370; M; 9.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
                                                                                                                                                                                                            Scott J.R., Pulliam W.M., Hollingshead S.K., Fischetti V.A.;
"Relationship of M protein genes in group A streptococci.";
Proc. Natl. Acad. Sci. U.S.A. 82:1822-1826(1985).
-I- FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SERVICE OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
M PROTEIN, SEROTYPE 6 PRECURSOR.
                                                                                                        CHAIN
                                                                                                                                              Virulence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=85166224; PubMed=3885219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 43-122 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
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 DOMAIN
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                                                                 DOMAIN
                                                                               TRANSMEM
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                                                                                                                                                                                                                                                                              send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL. SIMILARITY: TO OTHER M PROTEINS. SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROINTHE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ~
                                                                                                                                                                                                                                                                                                                                                                                                                                             PHAGOCYTOSIS.
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                                                                                                                                                                                                PF00746; Gram_pos_anchor; 1.
                                                                                                                                Phagocytosis;
ane; Coiled co
                          458
478
69
157
279
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                                       483
457
477
483
138
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                                                                                                                              Cell wall;
il; Signal.
BLOCKS SEPAN
                         10 X 7 AA TANDEM REPEATS.
4.5 X 25 AA TANDEM REPEATS.
TWO DIRECTLY REPEATED 27 AMINO
                                                                MEMBRANE AND
CYTOPLASMIC
                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                        PROTEIN,
            SEPARATED
                                                                                                                                            Duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483
                                                                            ANCHOR
                                                                                                     SEROTYPE
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                                                                 (POTENTIAL)
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                                                                                         ROTYPE 6. (POTENTIAL).
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             ВУ
             15 AMINO
                                                                                                                                              Repeat;
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                                                                                                                                              Antigen;
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             ACIDS
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Best Local (
                                                                                                                                                                                                                                                                                                                                         P19401;

P19401;

Ol-NOV-1990 (Rel. 16, Created)

Ol-NOV-1990 (Rel. 16, Last sequency

20-AUG-2001 (Rel. 40, Last annotaty

M PROTEIN, SEROTYPE 12 PRECURSOR
                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CS24 / Serotype M12;
MEDLINE=88058777; PubMed=2445730;
Robbins J.C., Spanier J.G., Jones
Robbins J.C., Spanier J.G., Jones
                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - \frac{1}{2}
                                                                                                                                                                                        sequences."
                                                                                                                                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                          M12_STRPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                  Bacteriol. 169:5633-5640(1987).
FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SERVOR PROTEIN M. PROTEIN M. IS CLOSELY ASSOCIATED WITH VIRULENCE THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         տ
                                                                             SUBCELLULAR LOCATION: TYPE I MEMBRANE SIMILARITY: TO OTHER M PROTEINS. SIMILARITY: TO OTHER STREPTOCOCCAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                               OF PROTEIN M. PROTEIN
THE BACTERIUM AND CAN
                                                              SIMILARITY: TO OTHER M PROTEINS.
SIMILARITY: TO OTHER STREPTOCOCCAL AN
IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                        PHAGOCYTOSIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELEESKKLTEKEKAELQAKLEAEAKALKEQLAKQAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFESVKNL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKEAIGTLKKTLDETVKDKIAKEQESK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHTDLGK-EGVTDADAKEAILKANGTKTKGAEELGKLFESVE--VLSKAAKEM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LANSYKELTSPYVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAV
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449
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454
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                                                                                                                                                                                                                                                                                                               Bacillus/Clostridium group;
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annotation update)
CURSOR (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKAAKEMLTNSVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 168.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68F87F28DB53A448
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                                                                                                                                                                                                   S.J., Simpson W.J., Cleaprotein gene regulation
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                                                                             AND STAPHYLOCOCCAL PROTEINS
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GRAM-POSITIVE COCCI
                                                                                                         PROTEIN. CELL WALL
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            he EMBL outstation restrictions on in
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                                                                                                                                                                SEROTYPES
                                                                                                                                                                                                     upstream
                                                                                                                                                                                                                     P.P.;
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European Bioinformatics Institute. T by non-profit institutions as long

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Query Match
                                                          SCAL_RICAK STANDARD: PRT; 998 AA. Q9ALX9; Q9ALX9; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) ANTIGENIC HEAT-STABLE 120 KDA PROTEIN (PS120)
                            Rickettsia akari
                                              (PROTEIN PS 120)
SCA4 OR D.
                                                                                                                                                                                                                                                                 374 KEL 376
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SEQUENCE
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TRANSMEM
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InterPro; IPR003345; M_repeat.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF02370; M; 9.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Virulence; Phagocytosis; Cell wall; Dupl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 LGKE---GVTDADAKEAI-LKANGTKTKGAEELGKLFESVEVLSKAAK--EMLANSVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 DLL----RHKQEIAEKENVIS-----KLNG-ELOPLKOKVD-----ETDRNLQQEKQKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M18269; AAA88573.1; -. PIR; A60115; A60115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                   TDDNAKKAILKTNNDKTKGADELEKLFESVKNL-----
                                                                                                                                                                                                                                                                                                                                                                          DHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HNEYQAKLAEKDGQIKQLEEQKQILDASRKGTARDLEAVRQAKKATEAELNNLKAELAKV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSPVVAESPKKPSMVN------NSGKDGNTSANSADESVKGPNLTE1SK-----KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSLEQQLAVTKENAKKDFELAALGHQLADKEYNAKIAELESKLADAKKDFELAALGHQHA
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                                                       (FRAGMENT).
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550
>564
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547
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62904 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.1%; Score 168.5; DB 1;
22.9%; Pred. No. 0.32;
tive 59; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                             -KKQVEKDLANLTAELDKVKEEKQISDASRQGLRRDLDASRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coil;
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COILED COIL (POTENTIAL).
GLY/PRO-RICH (CELL WALL-SPANNING)
CONSERVED IN GRAM-POSITIVE COCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M PROTEIN, SEROTYPE 12.
EXTRACELLULAR (POTENTIAL).
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                                                             (120 KDA ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 101;
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                                                                                                                                                                                                                                                                                                               -SKAAKEMLTNSV
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        RESULT 10
RBP2_PLAVB
ID RBP2_P
AC Q00799
DT 01-APR
DT 01-APR
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Best Local Similarity 20.7
Matches 102; Conservative
     RBP2_PLAVB
Q00799;
01-APR-1993
01-APR-1993
                                                                                                                              848 DISKIAIEKVNN
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NON_TER
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Phylogenetic analysis of Rickettsia spp. by comparing sequence gene D' coding for an intracytoplasmic protein."; Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sekeyova
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=786;
[1]
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                                                                                                                                                            NLSKAAKEMLTN 371
                                                                                                                                                                               GLKGQNLDEPKP--RDDIYNKAQDIAYALKNVVTTVLDANPEKREVSEEEVMNKTSSILN
                                                                                                                                                                                                                       KLKGEHTDLGKEGVTDDNAKKA------
                                                                                                                                                                                                                                                          SKGVDN-----
                                                                                                                                                                                                                                                                                                         ASHRTMAPTKKIAAIESVETGVAKSITDLEDKKLMTKGLVDGIYEDKANPEITSEMMKAV
                                                                                                                                                                                                                                                                                                                                                                      AFNTIAKTAAIQKVTTKVLDSPITAEIKGETLESITKIVAESPLNVQDKTDIVKGMGEAI
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                                                                                                                                                                                                                                                                                                                                       -----NAVVLAVKEVET-------LLTS-------IDELAKAI
                                                                                                                                                                                                                                                                                                                                                                                                             SANSADES-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVLSKAAKEMLANSV-----KELTSP------VVAESPKKPSMVNNSGKDGNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSSIDETAAKAIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGL--KEK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDAAKKCSETFTNKLKEKHTDLGKEGVTDADAKEAILKAN-GTKTKGAE--ELGKLFESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAGLTKEKDGNTQIDLINEAATAILNNEKEKQANFITLTKNMVNNNALTPDTKVARVNAV 483
   (Rel. 25, Created)
(Rel. 25, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z., Roux V., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            998
998 AA;
                                                STANDARD;
                                                                                                                                859
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; 109328 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.0%; Score 167.5; I
20.7%; Pred. No. 0.67;
tive 69; Mismatches
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sequence
                                              PRT;
                                                                                                                                                                                                                                           -STAIPEDKQALKDAAS-EAALDRA---TQNFTE
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                                              1251
                                                                                                                                                                                                               ---ILKTNNDKTKGADE--LEKLFESVK
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Gaps

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CHAIN

RESULT 9
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DT 20-AUG
DT 20-AUG
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Best Local S
Matches 91
MYS_AEQIR
P24733;
01-MAR-1992 (
01-MAR-1992 (
20-AUG-2001 (
MYOSIN HEAVY
                                                                                                                                                                                                  1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=92315338; PubMed=1617731;
Galinski M.R., Medina C.C., Ingra
                                                                                                                                          1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                merozoites."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, RETICULOCYTE BINDING |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M88098; AAA29744.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SP
HUMAN RETICULOCYTE CELLS.
SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE)
                                                                                                                                         EVNENTEMNTIESSAKEIEALYNELKNKKTSLNEIYQTSNEVK
                                                                                                                                                                                                                                                                                                                                         VVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNTNELDVHKNIQDAYKVALEI-----LAHSDEI------DTKQKDSSKL
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                                                                                                                                                                                                 VQDVLTLNEHFNTKQVSNHEPTNFDKSNKSSEELTKAVTDSKTIISK---
                                                                                                                                                                                                                           ISNLIT - - KKISAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAIL
                                                                                                                                                                                                                                                        ALDELLKKGRTCEVSRYKLIKDTVTKEISDDTELINTIEKNVK----AYLAYIKKNYEDT
                                                                                                                                                                                                                                                                                   SIDELAK------AIGKKIKNDVSLDNEADHNGSLISGAYL------
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                                                                                                                                                                      XTN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 22.6
91; Conservative
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1251 AA;
(Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 40, Last annotation updat
'Y CHAIN, STRIATED MUSCLE.
                                                                                                                                                                   NDKTKGADELEKLFESVKNLSKAAKEM--LTNSVK
                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Belem).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55;
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Pred. No. 0.
                                                                      PRT;
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J. Biol.
[2]
                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                      pfam; pF00063; myosin_head; 1.
pfam; pF01575; myosin_tall; 1.
pRINTS; PR00193; mYOSINHEAVY.
proDom; PD000355; myosin_head;
                                                                                                                                                                                                                                          EMBL; X55714; CAA39247.1; PIR; S13557; S13557. PIR; A40997; A40997.
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF MEDLINE-94173332; PubMed-8127365; Xie X., Harrison D.H., Schlichting I., Sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          muscle myosin heavy chain.";
Nucleic Acids Res. 18:7158-7158(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain. Sequence comparison with other heavy chains reveals that might be critical for regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aequipecten irradians (Bay scallop).
Eukaryota; Metazoa; Mollusca; Bivalvia;
Pectinoidea; Pectinidae; Argopecten.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Alkylation; Calmodulin-binding; 3D-structure.
                                          SMART; SM00015; IQ; 1
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resolution: implications for Structure 4:21-32(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Adductor muscle; MEDLINE-91088319; PubMed-2263488;
                            PROSITE;
                                                                                                                                                  InterPro;
                                                                                                                                                              InterPro;
                                                                                                                                                                                InterPro;
                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Houdusse A., Cohen C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96419133; PubMed=8805510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:306-312(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resolution
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nyitray L., Goodwin E.B., Szent-Gyorgyi i
"Nucleotide sequence of full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure of the regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure of the regulatory domain of scallop myosin at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vyitray L., Goodwin E.B., Szent-Gyoergyi A.G.;
Complete primary structure of a scallop striated muscle myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: MUSCLE CONTRACTION.

FUNCTION: MUSCLE CONTRACTION.

FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSIST HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (AMC-2).

SAND 2 REGULATORY LIGHT CHAIN SUBUNITS (MC-2).

SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                            rPro; IPR000048; IQ.
rPro; IPR002928; Myosin_tail.
rPro; IPR0022017; Spectrin.
rPro; IPR001609; myosin_head.
r) PF00612; IQ; 1.
                                                                                                                                                                                                              1WDC;
                                                                                                                                                                                                                            1SCM;
                             PS50096; IQ;
                                                                                                                                                                                                              30-APR-94.
11-JUL-96.
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tion.";
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
Hostetter M.K., Herman D.J., Kendrick K.E.;
                                            SEQUENCE OF 782-1790 FROM N.A
                                                                                                                              Nakajima H., Hirata A.,
Yamasaki M.;
                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetales;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                               01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.
USO1 OR INT1 OR YDL058W.
                                                                                         "A cytoskeleton-related gene, uso1, protein transport in Saccharomyces
                                                                                                                                         STRAIN-X2180-1A;
MEDLINE-91185402; PubMed-2010462;
" uirata A., Ogawa Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                       YEAST
                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                   NCBI_TaxID=4932;
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01-MAY-1992
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                                                                           transport in Saccharomyc
Biol. 113:245-260(1991).
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                         Bendel C.M.,
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Pred. No. 1.
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COILED COIL (POTENTIAL).
ATP (BY SIMILARITY).
ALKYLATION (SH-1) (BY SIMILARITY)
ALKYLATION (SH-2) (BY SIMILARITY)
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Best Local Similarity
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EMBL; L03188; AAB00143.1;
EMBL; U53668; AAB66659.1;
PIR; A38455; A38455.
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER
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     SNAVVLAVKEV - - -
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DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED OF AN HEPTAPETIBE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.

SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                           KEMLANSVKELTSPV--VAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITE
                                                                                              LETSEKALKEVKENEEHLKEEKIQLEKEATETKQQLNSLRANLESLEKEHEDLAAQLKKY
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                                                                                                                                                                                               LDGLKNEG------LKEKIDAAKKCSETFTNKLKE------
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S0002216; USO1
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ASP/GLU-RICH (ACIDIC).
G -> E (IN REF. 2).
E -> K (IN REF. 2).
V -> I (IN REF. 2).
V -> S (IN REF. 2).
I -> V (IN REF. 2).
I -> V (IN REF. 2).
G -> S (IN REF. 2).
G -> S (IN REF. 2).
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I -> V (IN REF. 2).
I -> V (IN REF. 2).
I -> D -> DEEDDEE (IN REF. 2).
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Pred. No. 1
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CHARGED (HYPER-HYDROPHII
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                           "X-ray structure of the magnesium(II).ADP.vanadate complex of the Dictyostelium discoideum myosin motor domain to 1.9-A resolution. Biochemistry 35:5404-5417(1996).
                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
MEDLINE-95345067; PubMed-7619796;
                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 1-762 MEDLINE-95345066; PubMed-7619795;
                                                                                                                                                                                                                                                       Wagle G., Noegel A., Scheel J., Gerisch G "Phosphorylation of threonine residues on Dictyostelium myosin heavy chain.";
                                                                                                                                                                                                                                                                                                        phosphorylatable heavy chain fragment of Dictyostelium myosin FEBS Lett. 269:239-243(1990).
                                                                                                                                                                                                                                                                                                                                                   STRAIN=AX2;
MEDLINE=90353583; PubMed=2387408;
STRAIN=AVANAMETER D., Schleicher M.,
                                                                                                                                                                                                                                                                                                                                                                                                          Warrick H.M., de Lozanne A., Leinwand L.A., 9 "Conserved protein domains in a myosin heavy Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum (Slime mold) Eukaryota; Mycetozoa; Dictyosteliida;
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X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) MEDLINE-97452580; PubMed-9305951;
                                                               X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
MEDLINE-96206189; PubMed-8611530;
                                                                                                             "X-ray structure of the magnesium(II)-pyrophosphate complex truncated head of Dictyostellum discoideum myosin to 2.7\text{-A}
                                                                                                                                 Smith C.
                                                                                                                                                                   "X-ray structures of the myosin motor discoldeum complexed with MgADP.BeFx aliochemistry 34:8960-8972(1995).
                                                                                                                                                                                                         Fisher A.J.,
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01-OCT-1989 (Rel. 12,
20-AUG-2001 (Rel. 40,
                                                      Smith C.A., Rayment
                                                                                                      resolution."
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                                                                                            34:8973-8981(1995).
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                                    1.9-A resolution.",
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of Mg.2'(3')-O-(N-methylanthraniloyl) nucleotides bound to t Dictyostelium discoideum myosin motor domain.";
J. Mol. Biol. 274:394-407(1997).
-I- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ACTIVITY THAT IS ACTIVATED BY ACTIN.
-I- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-AS INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC).
LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gulick A.M., Bauer C.B., Thoden J.B., Rayment "X-ray structures of the MgADP, MgATPgammas, a of the Dictyostelium discoldeum myosin motor d Biochemistry 36:11619-11628(1997).
use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                  This SWISS-PROT entry is copyright.
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PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION AND REDUCES THE ACTIN-ACTIVATED ATPASE ACTIVITY.

MISCELLANGOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EDTA ATPASE ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE OF A CYS AT THE SH-1
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MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN BE
SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
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European Bioinformatics Institute.
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SIMILARITY: CONTAINS 1
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DictyDb; DD01008; mhcA.
InterPro; IPR000048; IQ.
InterPro; IPR001609; myosin_head. Pfam; PF00063; myosin_head; 1. PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head; SMART; SM00015; IQ; 1. SMART; SM00242; MYSC; 1MNE; 1MND; A26655; A26655 S00250; S00250 PF00612; IQ; 1 M14628; ; PS50096; IQ; Coiled coil; P 17-AUG-96. 23-DEC-96. 28-JAN-98. 03-DEC-97. 17-AUG-96. 03-DEC-97. 03-DEC-97. 17-AUG-96 AAA33227.1; Actin-binding; ATP-binding; 3D-structure; Methylation; Alkylation; Phosphorylation. COILED ATP. METHYLATION (DI-) (POTENTIAL). ACTIN-BINDING ACTIN-BINDING NISOYM COIL HEAD-LIKE

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Arrota; Metazoa; Chordata;
Arria; Primates;
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P49454; Q13246; Q13171;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence upd
20-AUG-2001 (Rel. 40, Last annotation u
CENP-F KINETOCHORE PROTEIN (CENTROMERE
           MEDLINE-95379848; PubMed-7651420;
Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., Chen C.-F., Shan B.,
Jones D., Yang-Feng T.L., Lee W.-H.;
"Characterization of a novel 350-kilodalton nuclear phosphoprotein
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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kfein R.J., Mack G., Rattner J.B., Yen
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at late G2 and is rapidly degraded aft
130:507-518(1995).
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MEDLINE-98437347; PubMed-9763420;
Chan G.K.T., Schaar B.T., Yen T.J.;
"Characterization of the kinetochore binding interactions with the kinetochore proteins Ci
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DOMAIN
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EMBL; U30872; AAA82935.1; -.
EMBL; U25725; AAA86889.1; -.
HSSP; P02649; 11E4.
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-:- FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION,
-:- FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION,
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Li Q., Ke Y., Kapp J.A., Ferrtig N., Medsger T.A. Jr., C.
"A novel cell-cycle-dependent 350-kDa nuclear protein:
domain sufficient for nuclear localization.";
Biochem. Biophys. Res. Commun. 212:220-228(1995).
SEQUENCE
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                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE NUCLEOR REORGANIZATION TO THE KINETOCHORE/CENTROMERE (CORONAL SURRA THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS.

DEVELOPMENTAL STAGE: GRADUALLY ACCUMULATES DURING THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RETINOBLASTOMA PROTEIN (RB), C SUBUNIT: HOMO- OR HETERODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPERPHOSPHORYLATED DURING MITOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PhosphoryLation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Swiss
                                                                                                                                                                                                                                                                                         273
823
1642
1862
2207
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250
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611
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1611
1811
2242
2335
2492
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3210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
AA;
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                                         769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear
367589
                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen; Cell o
                                                        T -> A (IN REF. 2).
L -> Q (IN REF. 2).
G -> D (IN REF. 2).
MISSING (IN REF. 2).
MISSING (IN REF. 2).
V -> A (IN REF. 2).
V -> A (IN REF. 2).
ER -> DG (IN REF. 3).
L -> Q (IN REF. 3).
D -> N (IN REF. 2).
WW;
                                                                                                                                                                                                                                                                                                                                 COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
2 X 177 AA TANDEM REPEATS
        ELNERVAALHNDQEACK -:

(IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                          NUCLEAR LOCALIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G MITOSIS. INTERACTS
CENP-E AND BUBR1.
11D83324960E4334
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Centromere; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CENP-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain of CENP-E reveals
ENP-F and hBUBR1.";
                                           ţ
                                                                                                                                                                                                                                                                                                                                     REPEATS
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CRC64
                                           SSMREWQPCIMTKKPVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOLUS),
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                                                                                                                                                                                                                                                                          (POTENTIAL)
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Query Match
Best Local Similarity

8.8%; 21.8%;

Score Pred.

163;

DB .9;

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Length 3210;

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MYSB_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYSB_CAEEL P02566;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.C.

MEDLINE-83273600; PubMed-6576334;

Karn J., Brenner S., Barnett L.;

"Protein structural domains in the Caenorhabditis elegans
"protein structural domains in the Caenorhabditis elegans
"posin heavy chain gene are not separated by introns.";

myosin heavy chain gene are not separated by introns.";

myosin heavy chain gene are not separated by introns.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
MYOSIN HEAVY CHAIN B (MHC B).
UNC-54 OR MYO-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2313
                                                                                                                                                                              SEQUENCE OF 1876-1966 FROM N.A. MEDLINE-83232892; PubMed-6571695; Wills N., Gesteland R.F., Karn J.,
                                                                                                                                                                                                                                               "Periodic charge distributions match cross-bridge spacings in Nature 299:226-231(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2524
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                                                                                                                                                                                                                                                                                              McLachlan A.D., Karn J.
                                                                                                                                                                                                                                                                                                             MEDLINE-82272395;
                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 850-1966 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
                                                                                                                                    nonsense mutations via altered transfer
                                                                                                                                                 "The genes sup-7 X and sup-5 III of C.
                                                                                                                                                                  Waterston R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352
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FUNCTION: MUSCLE CONTRACTION.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                   33:575-583(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKV--QMKEKSSTAMEMLQTQLKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLKAKIEGMTQSLRGLELDVVTIRSEKEDLTNELQKEQERISELEIINSSFENILQEKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLCVLQQLK-----ESEHHADLLKGR--VENLERELEIARTNQEHAALEAENSKGEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEVHQLRRGIEKLRVRIEADEKKQLHIAEKLKERERENDSL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEVEALLSSIDEIAAKAIG---KKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKLFESVKNLSKAAKEMLTNSVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAKKCSEEFTAKLKGEHTDL-----GKEGVTDDNAKK-----AILKTNNDKTKGADEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLTSIDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KQIQEKQGQLSELDKLLSSFKSLLEEKEQAEIQIKEESKTAVEMLQNQLKELNEAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KANGTKTKGAEELGKLFESVEVL------SKAAKEMLANSVKELTSPVVAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RELQMSEENQELVILDAENSKAEVETLKTQIEEMARSLKVFELDL - - - - VTLRSEKENLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AALCGDQEIMKATEQSLDPPIEEEHQLRNSIEKLRARLEADEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                               PubMed=7202124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --EGLKEKIDAAKKCSETFTNKLKEKHTDLGKEGVTDADAKEAIL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                              in the muscle.
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                                                                                                                                                                                Barnett L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                                                                                myosin
                                                                                                                                    elegans
er RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147;
                                                                                                                                                                                                                                                                             rod amino acid sequence
                                                                                                                                                 suppress
                                                                                                                                                                                 Bolten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhabditoidea;
                                                                                                                                                   amber
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233

VVLAVKEVETLLTSIDELAKAIGKKIKN---

LAAE----LDGAQRDLRNTSTDLFKAKNAQE--ELAEVVEGLRRENKS-LSQEIKDLTDQ
VVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKK-------TTESNA

-GEGG----RSVHEMQKIIRRLEIEKEELQHALDEAEAALEAEESK

232 1569

----DVSLDNEADHNGSLISGAYL

280

VLRAQVEVSQIRSEIEKRIQEKEEEFENTRKNHARALESMQASLETEAKGKAELLR----

1528

1475

129

1415

LGKEGVTDADAKEAILKANGT---KTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSP

1527

128 1474 185

70

1358

1414

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ΩV
                                                                                            Query Match
Best Local
                                                                                                      MOD_RES
MOD_RES
MOD_RES
CONFLICT
                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002928; Myosin_ta:
InterPro; IPR001609; myosin_hee
Pfam; PF00063; myosin_head; 1
pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>-</del>
                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                         ATP-binding; Methylation;
                                                                                                                                                                                                                                                                                     SMART; SM00242; MYSC; 1.
Myosin; Muscle protein; Coiled coil; Thick filament;
                                                                                                                                                                                                                                                                                                 SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                ProDom;
                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0193;
                                                                                                                                                                                                                                                                                                                                                                                            PIR; A02992; MWKW.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J01050; AAA28124.1; -. EMBL; V01494; CAA24738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
                                                                                                                                                                      DOMAIN
                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                               DOMAIN
  16 SADESVKGPNLTEINKKITDSNAVLLAVK---EVEALLSSIDEI--AAKAIGKKIHQ-NN
                            Local Similarity 23.1 
les 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAN SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBFRAGMENT (S2)
                                                                                                                                                                                                                                                                                                                PD000355;
                                                                                                                                            851
1165
1165
177
665
769
128
                                                                                            A
                                                                                                                                                                                                                                                                                                                            MYOSINHEAVY
                                                                                                                                                                                                                        850
1966
1164
1176
                                                                                                                                                                                                                                                                                                             myosin_head;
                                                                                                        1880
                                                                                                                      1966
184
687
783
128
128
705
715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHC A AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS
                                        8.5%;
23.0%;
                                                                                                                                                                                                                                                                                                                                                             Myosin_tail myosin_head
                                                                                          225125 MW;
                                                                                                                                                                                                                                                                            Alkylation;
                             69;
                                                                                                      ALKYLATION (SH-1).
ALKYLATION (SH-2).
E -> R (IN REF. 2).
I -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHC B ARE
                                        Pred.
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Mismatches
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Sear Job	DЬ	Qy	В	Qy
ch com time:	1670	341	1626	281
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Result
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outer surface prot
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617.5	619	622	622.5	627	627	628	630	630.5	630.5	631	635.5	635.5	638	641.5	646
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S70259	140272	S69920	S69926	S69921	S69923	S69925	S70285	I40285	140281	S20543	140108	S70288	S70289	S70286	S69916
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ALIGNMENTS

outer surface prot C; Genetics:	surface prot surface prot surface prot surface prot surface prot	outer surface prot	surface prot	outer surface protein C - Lyme disea Outer surface protein C - Lyme disea C:Specles: Borrella burgdorferi (Lym C:Date: 13-Feb-1998 #sequence_revisi. C:Date: 13-Feb-1998 #sequence_revis	RESULT 1
	A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 19-210 <liv> A;Residues: 19-210 <liv> A;Coss-references: EMBL:L42887; NID:g858715; PIDN:AAB36995.1; PID:g1695212 A;Experimental source: strain Ip2</liv></liv>	A; Status: preliminary A; Molecule type: DNA A; Residues: 1-210 < JAU A; Residues: 1-210 < JAU A; Residues: 1-210 < JAU A; Cross-references: EMBL: X69596; NID: g311391; PIDN: CAAA9306.1; PID: g311392 A; Cross-references: EMBL: X69596; NID: g311391; PIDN: CAAA9306.1; PID: g311392 A; Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995 Mol. Microbiol. 18, 257-269, 1995 Mol. Microbiol. 18, 257-269, 1995 A; Title: Evidence for lateral transfer and recombination in OspC variation in Lyme di A; Reference number: S70255; MUID: 96296448	A;Reference number: 140209; MUID:90023102 A;Accession: 140209 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-210 https://documents.com/residues/no-number: DNA A;Reference number: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684 A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684 A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684 A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684 A;Title: Genetic heterogenity of the genes coding for the outer surface protein C (Os A;Reference number: S37726; MUID:93268136	G70218 Outer surface protein C - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000 C;Accession: G70218; 140269; S37726; S70281 C;Accession: G70218; 140269; S37726; S70281 R;Fraser, C.M.; Casjens, S.; Hunny, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997 A;Authors: Smith, H.O.; Venter, J.C. A;Au	

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                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, February 1994 A, Reference number: S72669 A, Mccession: S72669 A, Molecule type: DNA A, Residues: 1-124, 'D', 126-139, 'E', 141-210 < JAW>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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Pred. No. 4e-37;
3; Mismatches 1
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Query Match 45.9
Best Local Similarity 98.3
Matches 174; Conservative
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A;Gene: ospC
C;Superfamily:
                                                                                                                                                                                                                                           R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, J. Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrelia burgdorferi outer surface protection of the Borrelia burgdorferi outer surface protections in the surface protection of the Borrelia burgdorferi outer surface protections in the surface protection of the Borrelia burgdorferi outer surface protections in the surface protection of the surface protec
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                                                                                                                                   A; Cross-references;
                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-177 <RI
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R;Stevenson, B.; Barthold, S.W.
FEMS Microbiol. Lett. 124, 367-372, 1994
A;Title: Expression and sequence of outer surface pr
A;Reference number: 140143; MUID:95154673
A;Accession: I40144
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 19-210 <LIV>
A; Cross-references: EMBL:L42893; NID:g858721; PIDN:AAB37001.1;
A; Experimental source: strain 297
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 IKNDVSLDNEADHNGSLISGAYLISTLITKKISAIKDSGELKAEIEKAKKCSEEFTAKLK
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                             Lyme
                                                                                                                                                                 <RES>
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disease spirochete surface protein
                                                                                                                           EMBL: X84783;
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99.4%;
                                                                                             NID:9793825; PIDN:CAA59254.1;
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Pred. No. 4.3e-34;
0; Mismatches 1
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45.98;

Score 853; Pred. No. 5.

DB 2; .5e-33;

Length 177;

0,

Gaps

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Mismatches

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R; Livey, I; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A; Title: Evidence for lateral transfer and recombi
A; Reference number: S70255; MUID:96296448
A; Accession: S70279
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-193 < LIV>
A; Cross references: EMBL:L42898; NID:9858729; PIDN
A; Experimental source: strain 25015
C; Genetics:
A; Gene: ospC
C; Superfamily: Lyme disease spirochete surface pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: I40145
R; Stevenson, B.; Barthold, S.W.
R; Stevenson, B.; Barthold, S.W.
R; Stevenson, B.; Barthold, S.W.
Ltle: Expression and sequence of outer surface beference number: I40143; MUID:95154673
                                                                                                                                                                                        outer surface protein C - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_c;Accession: $70279
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A; Residues: 1-211 <RES>
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Best Local Similarity
Matches 158; Conser
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                                                                                                                                                                                                                                                                                                               KELTSPVVAESPKKP 211
                                                                                                                                                                                                                                                                                                                                           KELTSPVVAESPKKP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                  AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLITQKLGGLKNEELKEKIAAVKKCSEEFT
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81.0%;
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Pred. No. 2.7e-29;
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                                                                                                                                                  recombination
                                                             PIDN: AAB37007.1;
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outer surface protein C precursor - Lyme disease spirochete (strain PBre) C;Species: Borrelia burgdorferi (Lyme disease spirochete) A;Variety: strain PBre A;Variety: strain PBre C;Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000 C;Accession: S69918; S72674; I40103 C;Accession: S69918; S69
                                                                                                                                                              RESULT
S69918
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A;Title: Evidence for lateral transfer and recombination A;Reference number: S70255; MUID:96296448
A;Accession: S70287
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S70287
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A; Residues: 1-193 <LIV>
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A; Molecule type: I
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75.1%;
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81.9%;
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Pred. No. 5.9e-26;
7; Mismatches 3(
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Pred. No. 2.
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C;Superfamily: Lyme disease spirochete surface protein C
                                                                                                                                                                                                                                                                                 R:Fukunaga, M.; Hamase, A.
J. Clin. Microbiol. 33, 2415-2420, 1995
A:Title: Outer surface protein C gene sequence analysis of Borrelia burgdorferi sensu A:Reference number: 140269; MUID:96025162
A:Accession: 140277
A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                    outer surface protein C precursor - Borrelia afzelii
C.Species: Borrelia afzelii
te: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 26-May-2000
cession: I40277
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Best Local S
Matches 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Molecule type: DNA
A:Residues: 1-152,'E',154-211 <RC
A:Cross-references: EMBL:X81522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Clin. Microbiol. 33, 1860-1866, 1995
A;Title: Molecular analysis of genes encoding outer surface protein C (OspC) of Borrelia
A;Reference number: I40047; MUID:95395018
A;Accession: S69918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-211 < JAU>
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Best Local Similarity 77.6
Conservative
        119 TNKLKEKHTDLGKEGVTDADAKEATLKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
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|perfamily: Lyme disease spirochete surface protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 NKLKEKHTDLGKEGYTDADAKEAILKANGT-KTKGAEELGKLFESVEVLSKAAKEMLANS 178
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                                     AIGQKI-QNNGLAAEADKNGSLLAGAYAISTLIKQKLDGLKGLEGLNKEIAEAKKCSEAF 135
                                                        AIGKKIHONNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKN-EGLKEKIDAAKKCSETF 118
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                                                                                                                                                                         Similarity 74.5.46; Conservative
                                                                                                                                                                 37.3%; Score 692.5; DB 2; 74.5%; Pred. No. 1.5e-25; tive 20; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.4%; Score 695.5; DB 277.6%; Pred. No. 1.1e-25;
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22; NID:9872021; PIDN:CAA57242.1; PID:9872022
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A;Gene: ospC
C;Superfamily:
                                                                                         R;Margolls, N.; Hogan, D.; Cieplak, W. Gene 143, 105-110, 1994
A;Title: Homology between Borrelia burgdorferi OspC and A;Reference number: 140268; MUID:94259285
A;Accession: I40268
                                           A; Cross-references: GB:L25413; NID:g495735; PIDN:AAA22956.1; C; Genetics:
                                                                    A; Molecule type: DNA
A; Residues: 1-211 <R
                                                                                     A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                     outer surface protein C precursor - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
C:Accession: I40268
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C;Superfamily: Lyme disease spirochete surface protein
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A;Experimental source: strain ZS7
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A; Residues: 1-193 <LIV>
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Best Local Similarity 77,8%;
Matches 151; Conservative 1
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Pred. No. 1.7e-25;
.0; Mismatches 30
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Local Similarity 73.8 nes 144; Conservative

36.9%; Score 686.5; 73.8%; Pred. No. 2.9

Mismatches

); DB 2; 2.9e-25; hes 32;

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PID: 91041108

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C;Species: Borrelia afzelil
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997
C;Accession: 140273
R;Fukunaga, M, ; Hamase, A.
J. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence and A;Reference number: 140269; MUID:96025162
A;Accession: 140273
A;Status: preliminary; translated from GB/EMBL/DDF A;Molecule type: DNA
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S70273
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A:Molecule type: DNA
A:Residues: 1-190 <LIV>
A:Cross-references: EMBL:L42870; NID:g858737;
A;Experimental source: strain VSDA
C:Genetics:
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C:Superfamily: Lyme disease spirochete surface
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A;Title: Evidence for lateral transfer and record; R:Reference number: $70255; MUID:96296448
A;Accession: $70273
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Best Local Similarity
Matches 146; Conser
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pecies: Borrelia burgdorferi (Lyme disease spirochete)
ate: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000
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                  from GB/EMBL/DDBJ
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C;Superfamily:
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                                            RESULT
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A;Cross-references: GB:D49379; NID:g1041107; PIDN:BAA08377.1;
C;Superfamily: Lyme disease spirochete surface protein C
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A; Residues: 1-191 <LIV>
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Pred. No. 3.5e-25;
9; Mismatches 26;
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Search completed: March 18, 2002, 09:56:47 Job time: 370 sec
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R;Fung, B.P.; McHugh, G.L.; Leong, J.M.; Steere, A.C.
Infect. Immun. 62, 3213-3221, 1994
A;Title: Humoral immune response to outer surface protein C of Borrelia burgdorferi in A;Reference number: I40153; MUID:94314437
A;Accession: I40153
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-191 <RES>
A;Cross-references: EMBL:U08284; NID:9469561; PIDN:AAA21460.1; PID:9469562
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A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein C
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ALIGNMENTS

Query Match Best Local S Matches Q9S3P3 Q9S3P3; NON_TER NON_TER SEQUENCE Mol. Microbiol. 18:257-269(1995). EMBL; L42887; AAB36995.1; InterPro; IPR001800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1. ProDom; PD001149; Lipoprotein_6; 1. 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) OUTER SURFACE PROTEIN C (FRAGMENT). MEDLINE=96296448; PubMed=8709845; SEQUENCE FROM N.A. STRAIN-IP2; Bacteria; Borrelia burgdorferi (Lyme OSPC Livey I., Gibbs C.P., Schuster R., "Evidence for lateral transfer and NCBI_TaxID=139; Lyme disease Borrelia." 190; Similarity Spirochaetales; 192 192 AA; Conservative PRELIMINARY; 192 20287 MW; 50.7%; e disease spirochete). Spirochaetaceae; Borr Score 943; DB 2; Pred. No. 2.2e-36; 1; Mismatches 1 PRT; 11846F7AC84C7E3D CRC64; Dorner F.; recombination 192 B Borrelia ۲ Length 192; 'n Indels Ospc variation 0; Gaps 0

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123 KEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL 182

60

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Query Match
Best Local Similarity
                                                             MEDLINE=97478003; PubMed=9336916;
Ras N.M., Postic D., Foretz M., Baran
"Borrelia burgdorferi sensu stricto,
U.S.A.'?";
                                                                                                                                                                                                Q9R7B1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
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STRAIN=2-1498 CA4;

Probert W.S., Crawford M.R., Cadiz R.B., LeFebvre R.B.;

Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; L81131; AAB06569.1; -.

InterPro; IPR001800; Lipoprotein_6.

Pfam; PP01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.
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01-JUN-2001
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Bacteria; Spirochaetales; Spirochaetaceae; Bor
NCBL_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188;
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                                   Syst. Bacteriol.
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                                 47:1112-1117(1997)
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02, Last sequence update)
17, Last annotation update)
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Pred. No. 1.2e-35;
                                                                                             Baranton G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                       a bacterial
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Best Local Similarity
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SEQUENCE
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Marti-Ras N., Postic D., Foretz M., Br
Submitted (MAR-1997) to the EMBL/GenBr
EMBL, U91798; AABB1895.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                           InterPro; IPR001800; Lipoprotein_6; 1. Pfam; PF01441; Lipoprotein_6; 1. ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9RR53;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99091544; PubMed=9872945; Wang I.N., Dykhuizen D.E., Qiu W., Dunn J.J., Bosler E.M., Luft B.J., "Genetic diversity of ospc" in a local population of Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=OC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi (Lyme Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                  EMBL; AF029860; AAB86543.1; -
                                                                                                                                                                                                                                                                                                                                                                           Genetics 151:15-30(1999)
                                                                                                                                                                                                                                                                                                                                                                                        burgdorferi sensu stricto.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OUTER SURFACE
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NON_TER
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SEQUENCE FROM N.A.
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IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                               MACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA
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                                      1 MACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA
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                                                                                                                                                      Similarity
                                                                                                                                                                                                                                    193
193
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TremBLrel. 13, Created)
(TremBLrel. 13, Last sequence up
(TremBLrel. 17, Last annotation
DE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 AA;
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; 20297 MW;
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97.9%;
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97.9%;
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                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e disease spirochete)
Spirochaetaceae; Bor
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                                                                                                                        Score 908; DB Pred. No. 8.7e 3; Mismatches
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Pred. No. 2.2e-35;
3; Mismatches 1
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                                                                                                                                           DB 2;
3.7e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia
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T 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

OT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE OUTER SURFACE PROTEIN C (FRAGMENT).

OS Borrella burgdorferi (Lyme disease spirochete).

OS Borrella Spirochaetales; Spirochaetaceae; Borrelia
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01-MAY-2000 (TI
01-JUN-2001 (TI
OUTER SURFACE I
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Bacteria; Spirochaetales;
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80; Conservative
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(TremBLrel. 13, Last sequence update)
(TremBLrel. 17, Last annotation updat
DE PROTEIN C PRECURSOR (FRAGMENT).
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Pred. No. 4.4e-34;
3; Mismatches 1
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01-JAN-1998
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U.S.A.'?";
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  NON_TER
NON_TER
SEQUENCE
                             Wang I.-N., Dykhuizen D.E., Dunn J..
Submitted (OCT-1997) to the EMBL/Get
EMBL; AF029869; AAB86552.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                         SEQUENCE FROM N.A. STRAIN-OC10;
                                                                                                                               Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; S
                                                                                                                                                            01-JUN-2001 (TrEMBLrel. OUTER SURFACE PROTEIN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marti-Ras N., Postic D., Submitted (MAR-1997) to tlemBL; U91797; AABB1894.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97478003; PubMed=9336916;
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80; Conservative
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PD001149; Lipoprotein_6; 1.
191
191
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182 AA;
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(TrEMBLrel. 17, Last an
CE PROTEIN C (FRAGMENT).
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19202 MW;
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i sensu stricto, a bacterial
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to the EMBL/GenBank/DDBJ
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Spirochaetaceae; Bor
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EMBL/GenBank/DDBJ
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Query Match 47.6%; Best Local Similarity 100.0%; Matches 181; Conservative

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Score 885; DB 2; Pred. No. 9.6e-34;); Mismatches 0;

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Q44719;
01-NOV-1996
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Livey I., Gibbs C.P., Schuster R., Do.
"Evidence for lateral transfer and re-
tyme disease Borrella",
Mol. Microbiol. 18:257-269(1995).
EMBL; L42893; AAB37001.1; -
InterPro; IPRO01800; Lipoprotein_6.
Pfam: PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                        uery Match
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3P2
Q9S3P2
Q9S3P2;
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NON_TER
SEQUENCE
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01-MAY-2000
01-JUN-2001
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                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borr
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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(TrEMBLrel. 01,
                                                                                                                                                                                          192
192 AA;
             PRELIMINARY;
                                                                                                                                                        Conservative
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                    20472 MW; 46AC8F93E4DFED6C CRC64;
                                                                                                                                                    47.3%; Score 879; DB 2; 99.4%; Pred. No. 1.8e-33; tive 0; Mismatches 1
Created)
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T "Expression and sequence of outer surface protein C among N Marrican isolates of Borrelia burgdorferi.";

LL FEMS Microbiol Lett 124:367-372(1994).

PR EMBL; U04281; AAC43297.1; -

DR InterPro; IPR001800; Lipoprotein_6.

DR Pfam; PF01441; Lipoprotein_6; 1.

DR ProDom; PD001149; Lipoprotein_6; 1.

DR ProDom; PD001149; Lipoprotein_6; 1.

SEQUENCE 210 AA; 22526 MW; 2D672991D584E4EE CRC64;
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Best Local Similarity 99.4%;
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Q44999;
01-NOV-1996
01-NOV-1996
01-JUN-2001
                                    NON_TER
                                                                                                                      "Evolution of the Borrelia burgdorferi outer J. Bacteriol. 177:3036-3044[1995].
EMBL; X84783; CAA59254.1; [1907].
InterPro, IPR001800; Lipoprotein_6.
                 SEQUENCE
                                                                                   ProDom;
                                                                                                                                                                                                                                  Theisen M., Borre
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT).
                                                                                                    Pfam; PF01441;
                                                                                                                                                                                                                        Hansen K.;
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID=139;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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MEDLINE=95154673; PubMed=7851744;
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NCBI_TaxID=139;
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                                                                              PD001149;
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Lipoprotein_6; 1.
.49; Lipoprotein_6; 1.
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              ΑĄ,
  177
18800 MW;
                                                                                                                                                                                                                             M., Mathiesen M.J., Mikkelsen
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Spirochaetaceae; Borr
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156671B9614E7A2D CRC64;
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Pred. No. 2e-33;
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Query Match

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            O9R7B4 PRELIMINARY; PRT; 175 AA. 09R7B4; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 0UTER SURFACE PROTEIN C (FRAGMENT).

Borrella burgdorferi (Lyme disease spirochete).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
OUTER SURFACE PROTEIN C (FRAGMENT).
OSPC.
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Theisen M., Frederiksen B., Lebech A.M., Vuust J.,
"Polymorphism in ospC gene of Borrelia burgdorferi
immunoreactivity of OspC protein: implications for
use of OspC protein as a diagnostic antigen.";
J. Clin. Microbiol. 31:2570-2576(1993).
EMBL; X73622; CAA52001.1;
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
01-JUN-2001 (TREMBLR). 17, Last annotation updat
OUTER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrel
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Marti-Ras N., Postic D., Foretz M.,

Marti-Ras N., Postic D., Foretz M.,

Submitted (MAR-1997) to the EMBL/Ge

EMBL; U91792; AABB1889.1; -.

InterPro; IPR001800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6. 1.
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Ras N.M., Postic D., Foretz M., E
"Borrelia burgdorferi sensu stric
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1
                                                                                      Marti-Ras N., Postic D., Foretz M., Baranton (Submitted (MAR-1997) to the EMBL/GenBank/DDBJ EMBL; U91801; AAB81898.1;
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Lawson C.L., Swaminathan S.;
"Crystal structure of outer surface
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"Expression and sequence of outer surface protein C (
American isolates of Borrelia burgdorferi.";

FEMS Microbiol. Lett. 124:367-372(1994).

EMBL; U04282; AAC45540.1;

InterPro; IPR001800; Lipoprotein_6.

Pfam; PF01441, Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.
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MEDLINE=95154673; PubMed=7851744;
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ARBSULTI AABBOITI AAB Chimeric - Chimeric -03-APR-2001 (first entry) AAB62713 standard; Protein; Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick. Borrelia sp chimeric ospC protein SEQ ID NO: AAB62713; Borrelia sp. Borrelia sp. 377 Å

WPI; 2001-050113/06. N-PSDB; AAF29017.

Dattwyler RJ,

Seinost G,

Dykhuizen

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Luft BJ,

Gomes-Solecki M;

(UYNY) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC.

18-JUN-1999;

99US-0140042

19-JUN-2000; 2000WO-US16915

28-DEC-2000. WO200078966-A1

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                                                                                                    Borrelia; ospC; Lyme disease; vaccine; chimeric protein;
                                                                28-DEC-2000
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                                                                                                                  Borrelia sp chimeric
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Query Match
Best Local :
 19-JUN-2000;
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Chimeric -
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                                                                  WO200078966-A1
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98.18;
                                                                                                                                      disease;
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Pred. No. 1e-120;
2; Mismatches 2; 1
                                                                                                                                        vaccine;
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                                                                                                                                                                                            SEQ
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                                                                                                                                                                                               <u>N</u>O:
                                                                                                                                                                                            62
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                            Borrelia
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                                                                                                                                                                                                                                                                                                                                                                                                                               Compositions of OspC |
Lyme disease are used
to Lyme disease -
                                                                                                                                                                                                                                                                                                                                                Sequence
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03-APR-2001
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DB; AAF29033.
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                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                 Similarity
                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RJ,
                                                                                                                                                                                                                                                                                                                                                                                                               Page 125-126;
                                                                                                                                                                                                                                                                                                                                                397
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(first entry)
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                                Protein;
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97.98;
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d to immunize
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                                                                                                                                                                                                                                                                                                                                                                                                               160pp;
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                                 378
                                                                                                                                                                                                                                                                                                       Score 1793.5;
Pred. No. 1.9e
3; Mismatches
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detect immune
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                                                                                                                                                                                                                                                                                                                       22;
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18-JUN-1999;

Chimeric - Chimeric -

Borrelia;

Dattwyler RJ,

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121 KLKEKHTDLGKEGYTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leat to Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 43; Page 83-84; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease -
                                                                                                                                                                                                                                                                                                            NLAKAAKEMLANSVKEL 377
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|| nlskaakemltnsvkel 376
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BROOK BIOTECHNOLOGIES IN
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Borrelia
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                      Protein;
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87.8%;
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                      401
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Pred. No. 1.1e.
20; Mismatches
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                                                                                                    242
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                        205
                                                                                                                                           182
                                                                                                                                                               145
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                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Compositions of OspC p
Lyme disease are used
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Chimeric -
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                                                                                                                                                                                                                                                                                              Local
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                               \verb"eiekakkcseeftaklkgehtdlgkegvtddnakkailktnndktkgadeleklfesvkn"
                                                                     LTSPVVAESPKKDSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIE
                                                                                                              {\tt ltspvvaespkkpsmvnnsgkdgntsansadesvkgpnlteiskkitesnavvlavkeve}
                                                                                                                                                     1 \\ kekhtdlgkegvtdadakeailktngtktkgaeelgklfesvevlskaakemlansvke
                                                                                                                                                                | LKEKHTDLGKEGYTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE
                                                                                                                                                                                            326;
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                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              Page 150-151; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ospC; Lyme disease;
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86.7%;
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                                                                                                                                                                                                                                                                                22;
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                                                                                                                                                                                                                                                                                           Score 1589.5;
Pred. No. 7.2
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                                                                                                                                                                                                                                                                                Mismatches
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7.2e-106;
les 27; I
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                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                              Claim 43; Page 78-79; 160pp;
                                                                                                                                                                                                                                                                                                              Compositions of OspC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia;
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Borrelia
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                                                                                                                                                                          Score 1561; DB 22;
Pred. No. 7.1e-104;
2; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine;
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N-PSDB;
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Lyme disease are used
to Lyme disease -
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357 lskaakemltnsvkel 372
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hes 322;
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Pred. No. 1.3e-103;
3; Mismatches 27;
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                                                                                                                                                                                                                                                                                    Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                                                                                                                                                     Sequence
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Chimeric -
121 KLKEKHTDLGKEGVTDADAKEAILKANGT-KTKGAEELGKLFESVEVLSKAAKEMLANSV
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                                 GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLK-NEGLKEKIDAAKKCSETFTN 120
                                                                           ACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKAI
                      {\tt gkkikndgsldneanrnesllagaytistlitgklsklngseglkekiaaakkcseefst}
                                                                  acnnsgkdgntsansadesvkgpnlteiskkitdsnavllavkeveallssidel-akai
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                                                                                                            82.1%; Score 1519.5; DB 2
86.2%; Pred. No. 6.5e-101;
tive 10; Mismatches 31;
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Query Match Best Local S Matches

al Similarity 325; Conserv

Conservative

11;

Score 1516.5; Pred. No. 1.2e 11; Mismatches

.2e-100; es 31;

Indels

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Gaps

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                                                            The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea
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                                                      The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea
                                                                                                                                                                Claim 43;
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The present invention provides compositions comprising ospc proteins chimeric ospc proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leaves

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)B; AAF29039.
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                                                                                        43; Page 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia
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                                                                                                                                                                                                                                                          Dykhuizen
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                                                                                                                                                                                                                                                                                               INC.
                                                                                                                                                                                                                                                                                                              FOUND
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Best Local S
Matches 309
       Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease - \,
                                                N-PSDB;
                                                                            Dattwyler RJ,
                                                                                                                              18-JUN-1999;
                                                                                                                                                 19-JUN-2000; 2000WO-US16915
                                                                                                                                                                                        WO200078966-A1
                                                                                                                                                                                                            Chimeric -
Chimeric -
                                                                                                                                                                                                                                                         Borrelia sp chimeric ospC protein SEQ ID NO:
                                                                                                                                                                                                                                                                                 03-APR-2001
                                                                                                 (BROO-) BROOK
                                                                                                       (UYNY ) UNIV NEW YORK STATE RES FOUND
                                                                                                                                                                      28-DEC-2000
                                                                                                                                                                                                                                          Borrelia;
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                                                                                                                                                                                                                                                                                                                     AAB62726 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                          376
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DB; AAF29030.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 82.2
09; Conservative
                                                                                                                                                                                                                                        ospC; Lyme disease;
                                                                                                                                                                                                           Borrelia
Borrelia
                                                                                                                                                                                                                                                                              (first entry)
                                                                                               BIOTECHNOLOGIES
                                                                            Seinost
                                                                                                                             99US-0140042
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                                                                          Dykhuizen D,
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                                                                                                                                                                                                                                       vaccine;
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Pred. No. 7e-98;
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                                                                                                                                                                                                                                    chimeric protein; tick.
                                                                         Luft BJ,
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                                                                         Gomes-Solecki M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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WPI; 2001-050113/06
               Dattwyler RJ,
                                                                                                                        Chimeric -
Chimeric -
                                                         18-JUN-1999;
                             (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                      19-JUN-2000; 2000WO-US16915
                                                                                                        WO200078966-A1
                                                                                                                                                Borrelia; ospC; Lyme disease;
                                                                                                                                                                Borrelia
                                                                                                                                                                                 03-APR-2001
                                                                                                                                                                                                 AAB62724;
                                                                                                                                                                                                              AAB62724 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelli or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads to Lyme disease.
                                                                                                                                                                                                                                                          357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 43; Page 117-118; 160pp;
                                                                                                                                                                                                                                                                        362 LAKAAKEMLANSVKEL
                                                                                                                                                                                                                                                                                         297
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                                                                                                                                                                                                                                                                                            KIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVEN 361
                                                                                                                                                                                                                                                                                                                            TLLASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKE
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                                                                                                                       Borrelia
Borrelia
                                                                                                                                                               chimeric
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              Seinost
                                                       99US-0140042
                                                                                                                      sp.
                                                                                                                                                              ospC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.3%; Score 1467; [81.4%; Pred. No. 3.96 tive 30; Mismatches
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              G,
                                                                                                                                                              protein SEQ
              Dykhuizen
                                                                                                                                                                                                                560
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                                                                                                                                              chimeric protein;
             Luft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
3.9e-97;
hes 36;
                                                                                                                                                              NO:
                                                                                                                                                              52
             BJ,
             Gomes-Solecki M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                              tick.
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Matches 306
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Chimeric -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 43; Page 112-113; 160pp;
                                                                                                  Borrelia;
                                                                                                                Borrelia sp
                                                                                                                                   03-APR-2001
                                                                                                                                                                    AAB62737 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to Lyme disease.
        18-JUN-1999;
                        19-JUN-2000; 2000WO-US16915
                                                        WO200078966-A1
                                                                                                                                                    AAB62737;
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306; Conserv
                                                                                                 ospc;
                                                                        Borrelia
Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560 AA;
                                                                                                                 chimeric ospC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                  (first entry)
                                                                                                 Lyme
                                                                                                                                                                    Protein;
                                                                         дs
                                                                                                 disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.2%; Score 1465; I
81.0%; Pred. No. 8.80
Live 23; Mismatches
                                                                                                                                                                                                              375
                                                                                                                protein
                                                                                                  vaccine;
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                                                                                                  chimeric
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                                                                                                                                                                                                                                                                                                         rne present invention provides compositions comprising ospC proteins an chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads to Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                               Compositions of OspC p
Lyme disease are used
to Lyme disease -
                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                               Claim 43;
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ch l Similarity 224; Conser	36C-110 110, Application US 110, Application US 110, Application US 16248562 INFORMATION: ANT: Dunn, John J. ANT: Luft, Benjami OF INVENTION: No. OF INVENTION: Bori OF INVENTION: Bori FONDENCE ADDRESS: ESSEE: Brookhaven ET: UPton ET: UPton ET: UPton ET: UPton ET: UPTON MATYPE: Floppy di UTTRY: USA 11973 TRYE: Floppy di UTTRY: FORM: UTTRY: FORM: UTTRY: PC-DATION WARE: PAPPLICATION NUMBER: US NG DATE: 29-APR-19 WARE: PAPPLICATION DATA: ICATION NUMBER: US NG DATE: 01-11-93 EY/AGENT INFORMATION WIGHER: US NG DATE: 01-11-93 EY/AGENT INFORMATION EBOGOSIAN, MATGAT PHONNE: (516) 282-372 TON FOR SEQ ID NO: EGE CHARACTERISTICS: US MIND acid LOGY: linear UTH: 466 amino acid LOGY: protein 36C-110	77777777777777777777777777777777777777
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; MOLECULE TYPE: protein US-08-158-353-3
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Patent No. 5620862
                                                                                                                                                                                                                               TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAITOLI, Alice O.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                           TYPE: amino a STRANDEDNESS: TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,353
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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VENTION: Methods for Diagnosing Early Lyme
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Pred. No. 2.3e-64;
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                                                                                                                                                                                                                                                                                                                                                                                           Version
                                                                                     Length 210;
                                                            Indels
                                                           0;
                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15,
Patent No. 6
                                                                                                  DESCRIF N/A
HYPOTHETICAL: N/A
""T-SENSE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                           POSITION IN GENOME: FEATURE:
IDENTIFICATION METHOD: PUBLICATION INFORMATION:
                                                                                                                                                            TOPOLOGY: LINEAR MOLECULE TYPE:
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 10-MAR-CLASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: 3.5" FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                     LENGTH:
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CITY: N
                                                                                                                                                DESCRIPTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                       N/A
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FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
IMMEDIATE SOURCE:
LIBRARY: DSM 5662
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEPAX: (212) 557-5635
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/
FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WILSKE, BETTINA PREAC-MURSIC, VERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAR-1994
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amino acid analysis
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APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.001US2
CURRENT APPLICATION NUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER FILING DATE: 1994-03-10
EARLIER FILING DATE: 1992-06-19
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: US 08/209/02282
EARLIER APPLICATION NUMBER: DE 394 2728.5
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-06-13
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US-09-196-293-15
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Best Local Sim
Matches 189;
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                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09196293 Patent No. 6183755
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 16
SOOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 209
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                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                     IGKKIHONNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
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                                                                                                                                        ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
                                                                    IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                         Score 933; DB
Pred. No. 1.9e
3; Mismatches
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Pred. No. 7.9e-64;
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                                                                                                                                                                                                                           DB 4;
.9e-63;
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                                                                                                                                                                                                             Indels
                                                                                                                                                                                                             0;
                                                                                                                                                                                                           Gaps
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Patent No. 6
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                     Matches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MATGARET C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION: INFORMATION:
TETT-EDAME: 7516, 282-7738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (516) 282-37: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dunn, John J. APPLICANT: Luft, Benjamin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 ELTSPVVAESPK 208
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                                                                                                        121
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STATE: NY
COUNTRY: USA
ZIP: 11973
 197
                  181 ELTSPVVAESPKKP 194
                                                                    137
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                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
                                                                                                                                           77
                                                                                                                                                                                                              17 ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                 1 MACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
                                                                                     KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                            IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELTSPVVAESPK 192
                                                                  KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK
                                                                                                                                           IGKKIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
ELTSPVVAESPKKP
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6248562
                                                                                                                                                                                                                                                                                     Conservative
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282-3729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 6248562el Chimeric Proteins Comprising Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                     50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30:
                                                                                                                                                                                                                                                                                 Score 932; DB 4;
Pred. No. 2.2e-63;
3; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                        210
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                                                                                                                                                                                                                                                                                     Gaps
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RESULT

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TYPE: amino a TOPOLOGY: 1in MOLECULE TYPE: US-08-235-836C-122
                                                                                                            US-08-235-836C-107
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APPLICATION UNMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSLAN, MATGATE C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
TELEPHONE: (516) 282-3729
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acids
TYPE: BTIS COLUMN 1200
                                                           Sequence 107, Applicat Patent No. 6248562
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-235-836C-122
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   atches 191;
               TITLE OF INVENTION:
                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atent No. 6248562
GENERAL INFORMATION:
                                                                                                                                                                                                184 SPVVAESPKKPSMVNNSGKDGNTSANSADESVK 216
                                                                                                                                                                                                                                          406
                                                                                                                                                                                                                                              124 EKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT 183
                                                                                                                                                                                                                                                                                                                                                        346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrella Polypeptides and Uses Therefor
CUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            64 KIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETETNKLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/235,836C FILING DATE: 29-APR-1994 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Upton
STATE: NY
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                                                                                                                                                                  SPVVAESPKKPGTMAQYNQMHMLSNKSASQNVR 498
                                                                                                                                                                                                                                                                                           KIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETETNKLK
                                                                                                                                                                                                                             EKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT 465
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R P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         i: 588 amino acids
amino acid
                                                                                         Application US/08235836C
                           Dunn, John J.
Luft, Benjamin J
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SYSTEM: PC-DOS/MS-DOS
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   No. 6248562el Chimeric Proteins Comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                           50.2%;
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COUNTRY:
               STATE:
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US-08-158-353-2
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                                                                   Sequence 2, Application US/08158353
Patent No. 5620862
GENERAL INFORMATION:
APPLICANT: Padula, Steven J.
TITLE OF INVENTION: Methods for Diagnosing Early Lyme
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (516) 282-37.
INFORMATION FOR SEQ ID NO:
                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            456 SPVVAESPKKP 466
                                                                                                                                                                                                                                                                         184 SPVVAESPKKP 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          336 KIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 395
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                      ADDRESSEE: Hamilton, Brook, Smith & Reynolds, STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            64 KIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 11973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: BNL93-28A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bogosian, Margaret C
REGISTRATION NUMBER: 25,32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 29-APCLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal Similarity
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STATE: NY
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            Lexington
ΜĀ
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amino acid
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282-3729
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

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; MOLECULE TYPE:
US-08-158-353-2
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TELEPHONE: 617-861-9540
TELEPAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
"FNGTH: 212 amino acids
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Best Local Similarity 74.1%;
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                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08031295
Patent No. 5530103
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             08-031-295-2
                                                                                                                                                                                                                                          APPLICANT: LIVEY, IAN
APPLICANT: DORNUER, FREIDITCH
TITLE OF INVENTION: METHOD AND COMPOSITION FOR THE
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-Lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 SVKELTSPVVAESPKKP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 NKLKEKHTDLG--KEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLAN 177
                                                                                                                                                                                    ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington, D.C.
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REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UC
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                                                                                                                                                                        COUNTRY:
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             APPLICATION NUMBER: FILING DATE: 19930
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                                                                                                                                                        20007-5109
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Pred. No. 1e-44;
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US-07-903-580-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: LIVEY, Ian
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AN
TITLE OF INVENTION: PREVENTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/07/903,580

FILING DATE: 1926625
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LENGTH: 212 amino acids
TYPE: AMINO ACID
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APPLICATION NUMBER:
FILING DATE: 25-JUN-
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                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 VKELTSPVVAESPKKP 194
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                                                                                                                                                          COUNTRY: USA
ZIP: 22313-0299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202
TELEX: 904136
                                                                                                                                                                                                                     CITY: Alexandria
                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/727,245
                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MACNNSGKDGNT-SANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIGKKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDF
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                                                                                                                                                                                                    Virginia
                                                                                                                                                                                                                                      1800 Diagonal Road,
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                                                                                                                                                                                                                                                       Foley & Lardner
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                                                                                                                                                                                                                                                                                                              METHOD AND PREVENTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 670; DB 1;
Pred. No. 1.4e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                              COMPOSITION FOR OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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2.

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

NUMBER: US 07/727,245

APPLICATION NUMBER: US 0: FILING DATE: 22-JAN-1992

US 07/824,161

FILING DATE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 36.2%; Score 670; DB 4; Length 21 Best Local Similarity 73.0%; Pred. No. 1.4e-43; Matches 143; Conservative 15; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              equence 4, Application US/08158353 atent No. 5620862
                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-158-353-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: AMINO ACID
            ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
PEGISTRATION NUMBER: 33,542
                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,353
FILING DATE:
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Padula, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton,
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 VKELTSPVVAESPKKP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 TNKLKEKHTDLGKEGYTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELL. TELEFAX: 1... 899149
 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                            CITY: Lexington
                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 AIGKKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEG-LKEKIDAAKKCSETF 118
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                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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                                                                                                                                                                                                                                                                               Two Militia Drive
                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                              Steven J.
                                                                                                                                                                                                                                                                                                                                               Disease
                                                                                                                                                                                                                                                                                                                                                       Methods for Diagnosing Early Lyme
UCT93-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30472/131 IMMU
                                                                                                                                                                                                                                                                                         Smith & Reynolds, P.C
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; ORGANISM: Borrelia burgdorfer: US-09-196-293-11
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   Query Match
Best Local Similarity
Matches 138; Conserv
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                                                                                                                                                                           SOFTWARE: FastSEQ
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fuchs, R
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wilse, Bettina
APPLICANT: Wilse, Bettina
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
TILE REFERENCE: 738.001US2
CURRENT APPLICATION UNMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER FILING DATE: 1994-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11,
                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER FILING DATE: 1992-06-19
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                EARLIER FILING DATE: 1990-12-21

EARLIER APPLICATION NUMBER: DE P39 42 728.5

EARLIER FILING DATE: 1989-12-22

EARLIER APPLICATION NUMBER: DE P40 18 988.0
                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                              EARLIER FILING DATE: 1990-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fuchs, Renate APPLICANT: Motz, Manfred
                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-861-954U
INFORMATION FOR SEQ ID NO:
                                                                                                                                                         ENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 VKELTSPVVAESPKKP 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MACNNSGKDGNT-SANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1, Application US/09196293
6183755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soutscheck, Erwin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                           for Windows Version 4.0
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                     34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.1%; Score 631; DB 1; 69.9%; Pred. No. 1.3e-40;
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Score 629; DB 4; I
Pred. No. 1.8e-40;
.3; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
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                                   Length 212;
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                                                                                                                                                                                                                                                                                                               ILLEFAX: (212) 597-535;
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 212
TYPP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Applia Patent No. 6248538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: AT&T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS VERSION 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,603E
FILING DATE: 10-MAR-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WILSKE, BETTINA
APPLICANT: PREAC-MURSIC, VERA
APPLICANT: MOTZ, MANFRED
APPLICANT: SOUTSCHECK, ERWIN
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS
TITLE OF INVENTION: FROM BORRELIA BURGDORFERI
                                            ANTI-SENSOL.
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORIGINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: LK TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
                       IMMEDIATE SOURCE:
LIBRARY: DSM 5
                                                                                                                                                             HYPOTHETICAL: N/A
                                                                                                                                                                                                                      MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27.224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 VKELTSPVVAESPKKP 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/EP90/0228 FILING DATE: 21-DEC-1990 APPLICATION NUMBER: US 07/862,535 FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
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                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKELTSPVVAESPKKP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10016
                                                                                                                                                                                                                                                                                 AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08209603E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUCHS, RENATE WILSKE, BETTI
                       DSM 5662
                                                                                                                                                                                                                         PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        697-3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT/EP90/02282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKR-9217-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/08235836C Patent No. 6248562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 138;
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Best Local Similarity
                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/148
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSLAN, MATGATE C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                                                                                                             TELEFAX: (516) 282-37
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD: PUBLICATION INFORMATION: ANTI-SENSE: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dunn, John J.

APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 VKELTSPVVAESPKKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 TNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 29-APR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
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                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Brookhaven National Laboratory
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: NY
                                                                       amino acid
                                                                                                        212 amino acids
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70.4%;
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3; Pred. No. 1.8e-40;
13; Mismatches 43
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                                                                                                                                                       ; LENGTH: 209 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-235-836C-32
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; Sequence 32, Applicat:
; Patent No. 6248562
; GENERAL INFORMATION:
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                                                            Query Match
Best Local Similarity
Matches 133; Conserv
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                                                                                                                                                                                                                                                               TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 136; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
137 TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 VKELTSPVVAESPKKP 212
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ZIP: 11973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Upton
: NY

    Application US/08235836C
6248562

                                                                Conservative
                                                        33.2%; Score 614.5; DB 4; 68.2%; Pred. No. 2.2e-39; ative 20; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.8%; Score 626; DB 4 69.4%; Pred. No. 3e-40; tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 212;
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                                                          Indels
                                                                                          Length 209;
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                                                      Gaps
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Search completed: March 18, 2002, 09:55:33 Job time: 346 sec

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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maximum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tal number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                     Score
100.0
100.0
98.6
98.6
97.4
97.1
96.9
96.9
87.3
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Match
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cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
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Gapop 10.0 , Gapext 0.5
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1850
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                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
/cgn2_6/ptodata/2/paa/US088_COMB.pep:*
/cgn2_6/ptodata/2/paa/US089_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US086_COMB.pep:*
               US-09-596-746A-30
US-09-596-746A-82
US-09-596-746A-82
US-09-596-746A-26
US-09-596-746-62
US-09-596-746-62
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                                                                                                                                                                                                                                                                                     SUMMARIES
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168.507 Million cell updates/sec
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ALIGNMENTS

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OspC Chimera
US-09-596-746-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-596-746-30 ; Sequence 30, Application US/09596746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
Query Match 100.0%; Score 1850; DB 19; Best Local Similarity 100.0%; Pred. No. 3.4e-125; Matches 377; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                              SOFTWARE: 1
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APPLICANT:
APPLICANT:
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APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C: Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi
TITLE OF INVENTION: Borrelia afzelii That Cause Lym
FILE REFERENCE: 2631.1002-001
                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                     FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dattwyler, Raymond J.
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    Indels
                                           Length
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    0;
  Gaps
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Sequence

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1 MACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60

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APPLICANY: Dykhuize, Danial
APPLICANY: Luft, Benjamin J.
APPLICANY: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in I
FILE REFERENCE: 26311002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT APPLICATION NUMBER: US/09/596,746A
PRIOR APPLICATION WHEER: US/09-06-19
PRIOR APPLICATION WHEER: US 60/140,042
PRIOR APPLICATION WHEER: US 60/140,042
SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: OSPC Chimera
US-09-596-746A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-09-596-746A-30
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Best Local
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SEQ ID NO 30
LENGTH: 377
TYPE: PRT
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181 ELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEI 240
                                                                                                        61
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                                                                                                                                       Local Similarity
mes 377; Conserv
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                                        KLKEKHTDLGKEGVTDÅDAKEAILKANGTKTKGÅEELGKLFESVEVLSKÅAKEMLANSVK
                                                    KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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                                                                                       IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
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ilarity 100.0%;
Conservative (
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GENERAL IMPORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea
FILE REFERENCE: 2631,1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: OSPC C
US-09-596-746-82
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                                        362 LAKAAKEMLANSVKEL 377
                                                                                                          265 TILASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKE
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                  LAKAAKEMLANSVKEL
                                                          KIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVEN
                                                                       KIENAKKCSEDETKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVEN 361
                                                                                                                         TLLASIDELATKAIGKKIQONGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKE
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Scinost, Gerald.
APPLICANT: Scinost, Gerald.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzeili That Cause Lyme Disective Reference: 2631,1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
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US-09-596-746A-26
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TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in
FILE REFERENCE: 2631.1002-001
CUGRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
RUMBER: OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 82
LENGTH: 401
                                                                                                                                                                                   Sequence 26, Application US/09596746A GENERAL INFORMATION:
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Best Local Similarity
Matches 372; Conserv
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APPLICANT: Selnost, Gerald
APPLICANT: Dykhulzen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
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TYPE: PRT
ORGANISM: OSPC Chimera
-09-596-746A-82
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llarity 98.9%;
Conservative
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Pred. No. 2.4e-123;
2; Mismatches 2;
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; OTHER INFORMATION: OSPC Chimera
US-09-596-746A-26
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; OTHER INFORMATION: OSPC Chimera US-09-596-746-26
                                                                                                                                                             APPLICANT: DatLWyLL, APPLICANT: Seinost, Gerald APPLICANT: Seinost, Gerald APPLICANT: Dykhuizen, Danial APPLICANT: Luft, Benjamin J. APPLICANT: Maria J.C. Gomes-Solecki APPLICANT: Maria J.C. Gomes-Solecki TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Diametric Preference: 2631.1002-001
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SOFTWARE: Fas:
SEQ ID NO 26
FNGTH: 374
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                                                                         SOFTWARE: Fate SEQ ID NO 26 LENGTH: 373
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Best Local Similarity
                                                                                                                     CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
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NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
ORGANISM: Artificial Sequence
                            TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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                                                                                                           FastSEQ for Windows Version 4.0
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98.18;
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Pred. No. 1.1e-121;
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98.1%;

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APPLICANT: Dattwyler, Raymond J.

APPLICANT: Seinost, Gerald

APPLICANT: Luft, Benjamin J.

APPLICANT: Luft, Benjamin J.

APPLICANT: Maria J.C. Gomes-Solecki

TITLE OF INVENTION: Groups of Borrelia burgdorferi and

TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea

FILE REFERENCE: 2631.1002-001

CURRENT APPLICATION NUMBER: US/09/596,746

FURGENT FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: US 60/140,042

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 62

LENGTH: 397

TYPE: PRT
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US-09-596-746-62
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US-09-596-746-62
Sequence 62, Application US/09596746
GENERAL INFORMATION:
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GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTNK 121
                                           GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK
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Pred. No. 4.4e-121;
3; Mismatches 2;
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; SOFTWARE: FastSEQ for W:
; SEQ ID NO 62
; LENGTH: 398
; TYPE: PRT
; ORGANISM: ospC Chimera
US-09-596-746A-62
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APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.

APPLICANT: Luft, Benjamin J.

APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme I
FILE REFERRNCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/9/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-66-18
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Best Local Similarity
Matches 368; Conserv
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362 LAKAAKEMLANSVKEL 377
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                                                                    KIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVEN
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97.9%;
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Pred. No. 4.4e-121;
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383

LAKAAKEMLANSVKEL

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Sequence 28, Application US/09596746

GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
FILE REFERENCE: 2631.1002-001

CURRENT APPLICATION NUMBER: US/09/596,746

CURRENT FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR FILING DATE: 1999-06-18
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SOFTWARE: FASTSEQ FOR
SEQ ID NO 28
LENGTH: 378
TYPE: PRT
                                                                                                                                                 Sequence 28, Application US/09596746A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 87.3
Best Local Similarity 87.8
Matches 331; Conservative
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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87.8%; Pred. No. 3.66
tive 20; Mismatches
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hes 25;
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Best Local Similarity
Matches 331; Conserv
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SOFTWARE: FastSEQ for
SEQ ID NO 28
LENGTH: 378
                                                                  NUMBER OF SEQ ID SOFTWARE: FastSE SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                Sequence 80, Application US/09596746 GENERAL INFORMATION:
                                                                                                                                                                                      APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhulzen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
ORGANISM: OSPC Chimera
-09-596-746-80
                                                                                                                   CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/596,746A CURRENT FILING DATE: 2000-06-19 PRIOR APPLICATION NUMBER: US 60/140,042 PRIOR FILING DATE: 1999-06-18
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ORGANISM: Artificial Sequence
FEATURE:
                                    TYPE: PRT
                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 NLAKAAKEMLANSVKEL 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLKEKHTDLGKEGYTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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                                                      401
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FastSEQ for Windows Version
                                                                                     FastSEQ
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                                                                                     NOS:
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                                                                                      Windows Version
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Pred. No. 3.6e-108;
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APPLICANT: Dattryler, Raymond J.
APPLICANT: Scinost, Gerald
APPLICANT: Scinost, Gerald
APPLICANT: Scinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Huma
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
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US-09-596-746A-80
Sequence 80, Application US/09596746A
GENERAL INFORMATION:
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Best Local S
Matches 326
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122 LKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE
                                                       86
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                                                                                                                                                          / Match 85.9%; Score 1589.5; DB 19; Local Similarity 86.7%; Pred. No. 2.5e-106; Les 326; Conservative 22; Mismatches 27; Ir
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                                                       GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETNK 121
                                                                                               GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK 145
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                                                                                                                                                                                     Length 402;
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SEQ ID NO 24
LENGTH: 375
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local
                                                                                                                                                                                                                                                                                                                                                               Matches
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CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
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SOFTWARE: FastSEQ for Windows Version
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APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
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         297
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                                                                                                                                                                       KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
AEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVK
                        EKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVE
                                                                       ETLLASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLK
                                                                                                                               ELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGDNLTEISKKITESNAVVLAVKEI 240
                                                      ETLLTSIDELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELK
                                                                                                                 ELTSPVVAES----PAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEV
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Seinost, Gerald
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1.1e-104;
hes 27;
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US-09-596-746-60
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Sequence 60, Application US/09596746
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
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LENGTH: 374
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Best Local Similarity 85.9%;
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APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in
FILE REFERENCE: 2631.1002-001
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
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ORGANISM: Artificial Sequence
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|:||||||| ||||||
| LSKAAKEMLTNSVKEL 372
                                                                                                                                                                                                                                                                                     TLTSIDELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA
                                                                                                                                                                                                                     EIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKN
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; Pred. No. 2.6e-104;
22; Mismatches 27;
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Search completed: Job time: 972 sec

March

18,

2002,

10:08:44

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APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
FITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 60
LENGTH: 398
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                                                                                                                                                                                                                                                182 LTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIE 241
                                                                                                                                                                                                                                                                                                       145
                                                                                               302 KIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVEN
                                                                                                                                                  262 TLLTSIDELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA
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                                                                            GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK 121
                                                                                                                                                                                                                             LTSPVVAES----PAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVE
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/US00_NEW_COMB.pep:*

8: /cgn2_6/ptcdata/2/paa/US00_NEW_COMB.pep:*
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Match
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297.254 Million cell updates/sec
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US-09-974-992-3

US-09-708-427-19882

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US-09-742-096-5

US-09-742-096-3

US-09-708-427-3730

US-09-708-427-3729

US-09-708-427-32622

US-09-708-427-32622

US-09-708-427-32623

US-09-708-427-32623

US-09-708-427-32623

US-09-708-427-32623

US-09-708-427-32632

US-09-815-242-1296

US-09-815-242-1296

US-10-072-851-5639

US-09-815-242-5639

US-09-815-242-5639

US-09-815-242-5639

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 Sequence
 75, Appli
3, Appli
19883, A
19881, A
15520, A
15520, A
15590, A
15590, A
15639, A
16610, A
16610, A
16610, A
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Qy 179 VKELTSPVVAESPKKP 194 		1 MACNUSGKDGNTSANSADESVKGPULTEINKKITDSNAVLL ::	Query Match 37.4%; Score 692.5; DB 6; Length 211; Best Local Similarity 77.0%; Pred. No. 3.5e-43; Matches 151; Conservative 12; Mismatches 30; Indels 3;	RESULT 1 US-09-974-992-5 Sequence 5, Application US/09974992 SEQUENCE INFORMATION: APPLICANT: Mathlesen, Marianne J. APPLICANT: Mathlesen, Michael APPLICANT: Holm, Arne, APPLICANT: Ostergaard, Soren TITLE OF INVENTION: Novel OspC-derived peptide fragments FILE REFERENCE: 459-666P CURRENT APPLICATION NUMBER: US/09/974,992 CURRENT FILING DATE: 2001-10-10 PRIOR APPLICATION NUMBER: 09/180,089 PRIOR FILING DATE: 1999-05-13 PRIOR FILING DATE: 1997-05-02 NUMBER OF SEQ ID NOS: 40 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 5 LENGTH: 211 CORGANISM: Borrelia burgdorferi US-09-974-992-5	ALIGNMENTS	26 150.5 8.1 2434 6 US-09-815-242-5835 Sequence 27 150.5 8.1 2434 7 US-10-072-851-5835 Sequence 28 150 8.1 837 6 US-09-815-242-5883 Sequence 29 150 8.1 837 6 US-09-815-242-5883 Sequence 30 150 8.1 875 6 US-09-815-242-13080 Sequence 31 148.5 8.0 1313 6 US-09-708-427-1313 Sequence 31 148.5 8.0 1313 6 US-09-708-427-15044 Sequence 31 148.5 8.0 1313 6 US-09-708-427-15044 Sequence 31 148.6 8.0 3070 6 US-09-708-427-1267 Sequence 31 147.5 8.0 3170 6 US-09-708-427-21267 Sequence 39 145.5 7.9 1690 6 US-09-708-427-12166 Sequence 39 145.5 7.9 1690 6 US-09-614-150-10224 Sequence 42 142.5 7.7 1489 6 US-09-614-150-10311 Sequence 43 141.5 7.6 1725 7 US-10-037-182-12 Sequence 54 141.5 7.6 1786 7 US-10-037-182-12 Sequence 55 US-09-708-427-15046 Sequence 42 141.5 7.6 1786 7 US-10-037-182-10 Sequence 55 US-09-914-150-1636 Sequence 55 US-09-914-150-1636 Sequence 55 US-09-914-150-1636 Sequence 55 US-09-918-275-7 Sequence 55 US-09-914-150-1636 Sequence 55 US-09-918-275-7 Sequence 55 US-09-914-150-1636 Sequence 55 US-09-918-275-7 Sequence 55 US-0
	ω-ω ω	SSIDEIAAKA 60 : SSIDEL-AKA 75	211;	-		Sequence 5835, Ap Sequence 5883, Ap Sequence 5883, Ap Sequence 13080, A Sequence 13080, A Sequence 13044, A Sequence 7, Appli Sequence 7, Appli Sequence 21267, A Sequence 150445, A Sequence 150244, A Sequence 10224, A Sequence 15045, A Sequence 15045, A Sequence 10311, A Sequence 15045, Ap Sequence 15045, Ap Sequence 15045, Appli Sequence 15046, Appli Sequence 15046, Appli Sequence 67, Appli

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RESULT 2 US-09-974-992-7

Sequence 7, Application US/09974992 GENERAL INFORMATION:

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APPLICANT: OSTEMBARD, SOREN
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-02
I PRIOR APPLICATION NUMBER: PCT/DK97/00203
I PRIOR FILING DATE: 1997-05-02
I NUMBER OF SEQ ID NOS: 40
SOFTMARE: Patentin Ver. 2.1
LENGTH: 207
TYPE: PRT
COCCUMENT: 207

; ORGANISM: Borrelia
US-09-974-992-3
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               Query Match 32.2
Best Local Similarity 66.0
Matches 128; Conservative
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TYPE: PRT
ORGANISM: Borrelia afzelii
US-09-974-992-7
                                                                                                                                                                                                                                                                                                                                           Requence 3, Application US/09974992
ENERAL INFORMATION:
APPLICANT: Mathiesen, Marianne J.
APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
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Best Local :
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APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
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PRIOR ETILING DATE: 1999-05-13
PRIOR ETILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: DESCRIPTION:
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nes 137; Conservative
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                              32.2%; Score 596.5; 66.0%; Pred. No. 3.;
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             25; Mismatches
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                         .2e-36;
                                          DB 6;
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             38;
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FEATURE:

NAME/KEY: misc_feature

LOCATION: 1.1014

O'HER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1.1014

OTHER INFORMATION: Ceres Seq. ID 1836847

US-09-708-427-19883
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US-09-708-427-19883
; Sequence 19883, Application US/09708427
; GENERAL INFORMATION:
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Best Local Similarity
Matches 113; Conserv
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19883
LENGTH: 1014
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
270 GHNGTL-----LAGAYTISKLITQKLDGLK-NSEKLKEKIENAKKCSEDFTKKL--EG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
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                                                      690 VEKLKTHENQIEEYKKLAHEASGVADTRKVELEDALSKLKNLESTIEELGAKCQGLEKES
                                                                                                 234 VLAVKEIETLLASIDELATKAIG-----
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                                                                                                                                                                                                                                                                                                  95 KLDGLKNEGLKEKIDAA-----LKEKH 126
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Pred. No. 0.00018;
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; NAME/KEY: misc_feature
; LOCATION: 1..1018
; OTHER INFORMATION: Xaa is any ar
; NAME/KEY: misc_feature
; LOCATION: 1..1018
; OTHER INFORMATION: Ceres Seq. II
US-09-708-427-19882
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEO ID NOS: B5364
SOFTWARE: Patentin version 3.1
SEO ID NO 1982
LENGTH: 1018
TYPE: PRT
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Best Local :
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Pred. No. 0.00018;
B; Mismatches 161;
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: OTHER INFORMATION: Xaa is any
: NAME/KEY: misc_feature
: LOCATION: 1..1269
: OTHER INFORMATION: Ceres Seq.
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 19881
LENGTH: 1269
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Best Local Similarity
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ORGANISM: Arabidopsis thaliana
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                                    LTSKLQE 1125
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23.2%;
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Pred. No. 0.00024;
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Sequence 3, Application US/09742096
GENERAL INFORMATION:
APPLICANT: DAUBERSIES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STJ
FILE REFERENCE: 200773USODIV
CURRENT APPLICATION NUMBER: US/09/742,096
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION WHERE: US/09/73,642
PRIOR FILING DATE: 1998-02-06
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REQ ID NO 5
LENGTH: 630

TYPE: PRT
: ORGANISM: P. falciparum
US-09-742-096-5
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GENERAL INFORMATION:
APPLICANT: DRUILLE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 200773USODIV
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CURRENT FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 08/973,642
PRIOR FILING DATE: 1998-02-06
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PRIOR FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
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PRIOR FILING DATE: 1996-06-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 SETFTNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEEL--GKLFESV----EVL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 ESVAPSVEESVAEN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                KDSILNEIEEVKENVVTTILEKVEETTAESVTTFSNILEEIQENTITNDTIEEKLEELHE 455
                                                                                                                                                                                                                                                                                                                                                                    NVLSAALENTQSEEEKKEVIDVIEEVKEEVATTLIETVEQAEEESESTITEIFENLEENA
                                                                                                                                                                                                                                                                                                                                                                                                                  QL---GIENVTDENAKKAIL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VEESVAENVEEIVAPSVEESV--AENV 230
                                                                                                                                                                                                                                                                                                                                                                                                              -----ITDAAKDKGAAELEKLFKAVENLA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---EKIENAKKCSEDFTKKLEGEHA 322
                                                                                             STAGE POLYPEPTIDE MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144; Indels 104;
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CURRENT APPLICATION NUMBER: US/09/614,150
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
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US-09-614-150-6213
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PRIOR FILING DATE: 1996-06-12
PRIOR APPLICATION NUMBER: FR 95/07007
PRIOR FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 1786
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                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DETECTION KIT, SUCH AS TITLE OF INVENTION: ARRAYS, FOR DETECTING TITLE OF INVENTION: DROSOPHILA GENES.
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Best Local :
                                                    PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Venter, J. Craig APPLICANT: et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 VTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVVAES--P 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      588 EEIVAPTVEEI----VAPTVEEIVAPSVVESVAPSVEESVEENVEESVAENVEESVAENVE 644
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                                                                     APPLICATION NUMBER: 60/175,693 FILING DATE: 2000-01-12
                        APPLICATION NUMBER: 60/184,831 FILING DATE: 2000-02-24
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60/191,637
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Pred. No. 0.0031;
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EXPRESSION OF 10,000 OR MORE
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Sequence 3730, Application US/09708427

REMERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 3730
LENGTH: 805
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FASTSEQ for Windows VG
SEQ ID NO 6213
LENGTH: 1639
TYPE: PRT
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US-09-708-427-3730
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Best Local S
Matches 105
              NAME/KEY: misc_feature LOCATION: 1.805
OTHER INFORMATION: Xaa is NAME/KEY: misc_feature LOCATION: 1.805
OTHER INFORMATION: Ceres S
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les 105; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETFTNKLK-EKHTDLGKEGVTDADAKEAILKAN-----GTKTKG--AEELGK 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1 SEQ ID NO 3729 LENGTH: 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3729, Application US/09 GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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LOCATION: 1..841
                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa
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                      67
                                                       86 VKHKELTEVKEAFDGLGLELENSRKKMIELEDRIRISALEAEKLEELQKQSASELEEKLK 145
                                                                                          21 VKGPNLTEINK-----KITDSNAVLLAVKE---VEAL----LSSIDEIAAKAIGKKIH
                                                                                                                             Local Similarity
nes 86; Conserv
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QNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKI-------
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FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..1038

OTHER INFORMATION: Xaa is any an NAME/KEY: misc_feature
LOCATION: 1..1038

OTHER INFORMATION: Ceres Seq. II
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US-09-708-427-32624
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Best Local Similarity
Matches 104; Conserv
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32624
LENGTH: 1038
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NGEIIKPCEAKENREQPAKKSFTEEE-----AARIIQSMYRGYDVRRWEPIKKLKEIAT 593
                                    LANSVKELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLT--EISKKITESNA 232
                                                                           AAPLSSKKAESRTVPEACNVKCEDANAEMKMAEGSLNALRTEKG----SVESNSNLQEES
                                                                                                           SETFINKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEM 174
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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TYPE: PRT
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SDTNLEKVLRLSPEEHPMSVLNRTDEKQAESAAETEEGYGLFETLATDSKQATENA
                                                                             ALATELSSIQDKLDSLKNSCASAEKEAVKEQVEIKSQPSD---SPVNLEHSQLTEENKMV
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7 25.0%;
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NAME/KEY: misc_feature

LOCATION: 1..1043

OTHER INFORMATION: Xaa is any amino ac

NAME/KEY: misc_feature

LOCATION: 1..1043

OTHER INFORMATION: Ceres Seq. ID 1834(
                                                                                                                                                                          Sequence 7646, Application US/10032585
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.4
Best Local Similarity 25.0
Matches 104; Conservative
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SEQ ID NO 32622
LENGTH: 1043
TYPE: PRT
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7646
                                                                                                            APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies
FILE REFERENCE: 10182-005-999
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25.0%; Pred. No. 0.0032;
htive 53; Mismatches 186;
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; OTHER INFORMATION: X=any
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                                  356 FKAVENLAKAAKEMLANSVKEL 377
                                                                                                                                                                                          247 IDELA--TKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKN--SEKLKEK 302
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LELLKNDNSGAKKELSEKVSKL 1855
                                                                                                              IENAKKCSE---DFT---KKLEGEHAQLG-IENVTDENAKKAILITDAAKDKGAAELEKL 355
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Search completed: March 18, 2002, 09:58:21 Job time: 379 sec

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	٥
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33.6	33.9	33.9	33.9	34.1	34.1	34.1	34.1	34.4	34.4	34.5	34.7	34.9	35.1	35.4	30.0
209	212	210	210	192	209	209	212	203	191	194	193	214	212	212	607
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S69926	S69921	S69923	S69925	S70285	I40285	I40281	S20543	I40108	S70288	S70289	S70286	S69916	I40143	I40279	140147
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R.Fukunaga, M.; Hamase, A.
J. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence analysis
A;Reference number: I40269; MUID:96025162
A;Accession: I40269
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000
C;Accession: G70218; I40269; S37726; S70281
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
                                                                            A; Experimental source: strain C; Genetics:
                                                                                                A; MOLECULE LIFT.
A; Residues: 19-210 <LIY>
A; Cross-references: EMBL: L42887; NID: g858715;
A; Cross-references: Experimental source: strain Ip2
                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X69596; NID:g311391; PIDN:CAA49306.1; PID:g311392 R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995 Mol. Microbiol. 18, 257-269, 1995 A;Title: Evidence for lateral transfer and recombination in OspC variation A;Reference number: S70255; MUID:96296448 A;Accession: S70281 A;Status: nucleic acid sequence not shown
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A;Residues: 1-210 <RES>
A;Residues: 1-210 <RES>
A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684
A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684
R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschek, Med. Microbiol. Immunol. 182, 37-50, 1993
Med. Microbiol. Immunol. 182, 37-50, 1993
A;Title: Genetic heterogenity of the genes coding for the outer surface protein C A;Title: Genetic heterogenity of the genes coding for the outer surface protein C A;Reference number: S37726; MUID:93268136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943
A;Accession: G70218
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A; Residues: 1-210 <KI
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A; Residues: 1-210 < J/
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Superfamily: Lyme disease spirochete surface
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A;Reference number: S72669
A;Accession: S72669
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
A;Variety: strain PKa
C;Date: 15-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-May-2000
C;Accession: S69927; S72669
R;Jauris-Helpke, S; Liegl, G; Preac-Mursic, V.; Roessler, D.; Schwab, E.; Soutschek, J. Clin. Microbiol. 33, 1860-1866, 1995
A;Reference number: I40047; MUID:95395018
A;Accession: S69927
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-124,'D',126-139,'E',141-210 <JAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Status: nucleic acid sequence not shown A:Molecule type: DNA A:Residues: 1-210 <JAU> A;Cross-references: EMBL:X69589 A:Experimental source: Strain PKa R:Jauris, S.
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uperfamily: Lyme disease spirochete surface protein
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                                                 ELTSPVVAESPKKP 210
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                                                                                                                                                            IGKKIHONNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETN 120
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Similarity 96.9%;
88; Conservative
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97.9%;
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Pred. No. 1.
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Pred. No. 5.5e-39;
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A; Residues: 1-193 <LIV>
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178; Conserv
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C;Accession: I40153
R;Fung, B.P.; McHugh, G.L.; Leong, J.M.; Steere, A.C.
Infect Immun. 62, 3213-3221, 1994
A;Title: Humoral immune response to outer surface protein A;Reference number: I40153; MUID:94314437
A;Accession: I40153
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C;Superfamily: Lyme disease spirochete surface protein
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A;Residues: 1-191 <RES>
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Best Local Similarity 100.0%; Pred. No. 100.0%; Pred. 
                                       319 GEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL
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                                                                                                                                             IQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLE
                                                                                                                                                                                IQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLE 318
                                                                                                                                                                                                                                                                                              NSGKGGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLÄSIDELATKAIGKK
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Pred. No. 4.2e
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4.2e-35;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-178 <RES>
Cross-references: EMBL:X84779; NID:g793817; PIDN:CAA59250.1; PID:g793818
C;Superfamily: Lyme disease spirochete surface protein C
                                                                                                                                                                                                                                                                                                                                                                                                  outer surface protein C - Lyme disease spirochete (strain MUL) (fragment) c;Species: Borrella burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-200 C;Accession: I40125; S54195
C;Accession: I40125; S54195
C;Theisen, M.; Borre, M.; Mathlesen, M.J.; Mikkelsen, B.; Lebech, A.M.; H; J. Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrella burgdorferi outer surface protein OspC
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Best Local Similarity
Matches 174; Conserv
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                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                205 NTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGKKIQQNGG
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 121
                                                                                   265 LAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQL
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                                                                                                                                   1 NTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGKKIQQNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVV 187
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GIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL 377
                                                                LAVEAGHNGTSLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKEKHTDLG
                                                                                                                                                                                                                   Similarity
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98.3%;
                                                                                                                                                                                                                 98.88;
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Pred. No. 1.1e-34;
                                                                                                                                                                                                                 Score 826; DB 2;
Pred. No. 2.3e-33;
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 173
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outer surface protein C - Lyme disease spirochete (strain 272) (fragment) C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000 C;Accession: I40104; S54184 R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, A.M.; Hans J. Bacteriol. 177, 3036-3044, 1995 A;Title: Evolution of the Borrelia burgdorferi outer surface protein OspC. A;Reference number: I40104; MUID:95286481 A;Accession: I40104
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C; Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Stevenson, B.; Barthold, S.W.
FEMS Microbiol. Lett. 124, 367-372, 1994
A;Title: Expression and sequence of outer
A;Reference number: I40143; MUID:95154673
A;Accession: I40145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Borrelia burgdorferi (Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change C;Accession: I40145
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A; Residues: 1-178 < RI
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A; Residues: 1-211 <RES>
A; Cross-references: EMBL:U04282; NID:g2314881; PIDN:AAC45540.1;
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Best Local Sim
Matches 170;
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Best Local
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    180
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                                                                                                                                                                                                 17 ISCNNSGKDGNAASTNPADESVKGPNLTEISKKITDSNAVVLAVKEVGALLTSIDELATK
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                                                                                                                                         AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFT 119
                                                                                                                     AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLITQKLGGLKNEELKEKIAAVKKCSEEFT
    KELTSPVVAESPKKP 194
                                         NKLKSSHTELGKQDAQDDDAKKAILRTHNTKDKGAEELDKLFKAVENLSKAAKEMLSNSV
                                                                              NKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSV
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Pred. No. 3.2e-33;
Pred. No. 3.2e-33;
                                                                                                                                                                                                                                                                                               Score 774.5; DB 2
Pred. No. 8.1e-31;
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                                                                                                                                                                                                                                                                                                                      211;
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C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-
C; Accession: I40124; S54194
R; Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, A
J; Batteriol. 177, 3036-3044, 1995
A; Title: Evolution of the Borrelia burgdorferi outer surface protei
A; Reference number: I40104; MUID:95286481
A; Accession: I40124
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-178 <RES>
A; Cross-references: EMBL:X84782; NID:9793815; PIDN:CAA59253.1; PID:
C; Superfamily: Lyme disease spirochete surface protein C
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C;Superfamily: Lyme disease spirochete surface
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S70279
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                                                                                                                               Query Match
Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA
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   1265
                                                                                205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 LTSPVVAESPKKP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 LKEKHTDLGKEGVTDADAKEAILKANGTKTKGABELGKLFESVEVLSKAAKEMLANSVKE 181
                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
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                                LAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTSPVVAESPKKP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNNSGKDGNAASTNPADESYKGPNLTEISKKITDSNTVVLAVKEVEALLTSIDELATKAI 60
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58; Conservative
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid sequence not shown
                                                                                                                            39.9%;
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81.9%;
                                                                                                        Score 739; DB Pred. No. 3.3e 6; Mismatches
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Pred. No. 8.2e-31;
ll; Mismatches 23;
                                                                                                                          DB 2;
.3e-29;
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                                                                                                                                      Length 178
                                                                                                        Indels
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                                                                                                                                                                                                       PID: 9793816
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                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                    0;
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Outer surface protein C precursor - Lyme disease spirochete (strain PBre) C;Species: Borrelia burgdorferi (Lyme disease spirochete) A;Variety: strain pBre A;Variety: strain pBre B;Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-20;Accession: S69918; S72674; 140103 R;Jauris Heipke, S; Liegl, G; Preac-Mursic, V.; Roessler, D.; Schwab, E J. Clin. Microbiol. 33, 1860-1866, 1995 A;Title: Molecular analysis of genes encoding outer surface protein C (Os) A:Poference Sumber: 1401017. MITT.06796709
A;Reference number: 140047; MUID:95395018
A;Accession: S69918
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                    S69918
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A; Residues: 19-210 <LIV>
A; Cross references: EMBL:L42893; NID:g858721;
A; Cross references: strain 297
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C;Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U04281; NID:g434663; PIDN:AAC43297.1; PID:g434664 R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995 A;Title: Evidence for 157-269, 1995 Transfer and recombination in OspC variation
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A; Residues: 1-210 < RES>
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ilarity 75.4%;
Conservative 2
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Pred. No. 1.1e~27;
22; Mismatches 24
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A; Residues: 1-211 <JAU>
A; Cross references: EMBL:X81522; NID:g872021; PIDN:CAA57242.1; PID. A: Experimental source: strain PBre R; Roessler, D.
submitted to the EMBL Data Library, September 1994
A; Reference number: S72674
A; Accession: S72674
A; Molecule type: DNA
A; Residues: 1-152, 'E', 154-211 <ROE>
A; Cross-references: EMBL:X81522; NID:g872021; PIDN:CAA57242.1; PID C; Gene:Los:
A; Gene: OspC
C; Superfamily: Lyme disease spirochete surface protein C
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J. Clin. Microbiol. 33, 2415-2420, 1995

A;Title: Outer surface protein C gene sequence analysis
A;Reference number: I40269; MUID:96025162

A;Accession: I40277
A;Cession: I40277
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Matches 146; Conserv
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                               VKELTSPVVAESPKKP 194
                                                                                                                  AIGOKI-QNNGLAAEADKNGSLLAGAYAISTLIKQKLDGLKGLEGLNKEIAEAKKCSEAF
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152; Conservative
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Pred. No. 4.9e-27;
2; Mismatches 29
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Pred. No. 6.9e-27;
0; Mismatches 27;
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Gene 143, 105-110, 1994
A.Title: Homology between Borrelia burgdorferi
A.Reference number: 140268; MUID:94259285
A;Accession: I40268
A;Status: preliminary; translated from GB/EMBL/
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R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
Rol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination
A;Reference number: $70255; MUID:96296448
A;Accession: $70280
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I40268
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change
                                                                                                                                                                      A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
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A; Residues: 1-211 <RES>
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A; Residues: 1-193 <LIV>
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                                                                           Query Match
Best Local S
Matches 144
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Best Local Similarity
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LKEKHTDLGKEGVTDADAKEAILKANGT-KTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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73.8%;
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                                                                         Score 686.5; DB 2;
Pred. No. 1.3e-26;
.8; Mismatches 32;
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Pred. No. 7.7e-
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Q10419 strepticoccc
Q99323 drosophila
P24733 aequipecten
P02566 caenorhabdi
P39216 baccillus su
P08799 dictyosteli
P24043 homo sapien
Q9aj81 rickettsia
P49454 homo sapien
P19401 strepticococc
P47037 saccharomyc
Q9aix9 rickettsia
P49454 homo sapien
Q00798 plasmodium
P42384 mycobacteri
Q21313 caenorhabdi
P31111 saccharomyc
P02469 mus musculu
P30622 homo sapien
Q9aj83 rickettsia
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P80200 helicobacte
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reliton E.F. D., S.,	Soutschek an immuno ."; Ryan R.W.; OspC) from	Schwab	049419 090339 008696 P12270 P35380 P35217 P93203 P16952 P40767 P47035
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burgdorferi.";
Nature 390:580-586(1997).
-!- FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.
-!- FUNCTION: NOT KNOWN; ATTACHED TO THE OUTER MEMBRA
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1
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EMBL; AE000792; AAC66329.1; --
TIGR; BBB19; --
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R EMBL; X62162; CAA44093.1; -.

R EMBL; X73624; CAA52003.1; -.

R InterPro; IPRO01800; Lipoprotein_6; 1.

R Pfam; PF01441; Lipoprotein_6; 1.

R ProDom; PD001149; Lipoprotein_6; 1.

W Outer membrane; Lipoprotein; Signal; Plasmid; Antigen.

T SIGNAL 18 BY SIMILARITY T

T CHAIN 19 212 OUTER SURFACE PROTEIN C.

T LIPID 19 19 N-ACYL DIGLYCERIDE (BY SIMI: C2006C331FBF2E7D4 CRC64;
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Best Local
                                                                                                                                                                              VM24_BORHE
P32778;
01-OCT-1993
                                                                                                                                           01-OCT-1993
01-FEB-1994
                              NCBI_TaxID=140;
                                                Bacteria; Spirochaetales;
                                                                       Plasmid.
                                                                                       Borrelia hermsii.
                                                                                                            VMP24
                                                                                                                           VARIABLE
SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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J. Clin. Microbiol. 31:2570-2576(1993)
-I- FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94075528; PubMed=8253951;
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STRAIN=DK26;
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Mol. Microbiol. 6:503-509(1992).
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137; Conserv
                                                                                                                  993 (Rel. 27, Created)
993 (Rel. 27, Last Sequence update)
994 (Rel. 28, Last annotation update)
MAJOR OUTER MEMBRANE LIPOPROTEIN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                 STANDARD;
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                                              Spirochaetaceae;
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Mismatches
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.6e-23;
                                                                                                                    PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
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Best Local S
Matches 91
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EMBL; L04786; AAA...

InterPro; IPR001800; Lipoprotein_6; 1.

Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein; 1.

PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

PROBABLE.

VARIABLE MAJOR OUTER MEM

TROPROTEIN 24.

                                                                                                                                                                                                                                                                                                        VM03_BORHE
Q02448;
Q1-JUL-1993
Q1-JUL-1993
Q1-FEB-1994
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Restrepo B.I., Kitten T., Carter C.J., Infante D., Barbour A "Subtelomeric expression regions of Borrelia hermsil linear are highly polymorphic.",
Mol. Microbiol. 6:3299-3311(1992).
-I- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHEROM ONE SURFACE EXPOSED VMP TO ANOTHER.
SEQUENCE FROM N.A.
STRAIN-SSP, HS1 SEROTYPE 3;
MEDLINE-93133110; PubMed=1484486;
Restrepo B.I., Kitten T., Carter C.J.,
"Subtelomeric expression regions of Bor
                                                                                                                                                                                                                                                                                                                                                                                                                                        BORHE
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                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                           Plasmid
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                                                                                                                                                                                                                                                               VMP3.
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                                                                                                                                                      NCBI_TaxID=140
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214 /
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(Rel. 26, Last sequence update)
(Rel. 28, Last annotation update)
JOR OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR
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                                                                                                                                                                                Spirochaetaceae;
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Pred. No. 3.2e-12;
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     Borrelia
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     Infante D., Barbour /
rrelia hermsii linear
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                               Barbour A.G.;
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Best Local S
Matches 92
                                                               SEQUIENCE FROM N.A.
SEQUIENCE FROM N.A.
MEDLINE-87308395; Pubmed-3040773;
MEDLINE-87308395; Pubmed-3040773;
Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.;
Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.;
Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.;
Committee nucleotide sequence and deduced polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Euro
           01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
MYOSIN II HEAVY CHAIN, NON MUSCLE.
Acanthamoeba castellanii (Amoeba).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are highly polymorphic.";

Mol. Microbiol. 6:3299-3311(1992).

-i- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.

-i- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                              Eukaryota; Acanthamoebidae; Acanthamoeba
                                                                                                                                                                                                                                                                              MYSN_ACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Outer membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01441; Lipoprotein_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L04789; AAA22967.1; -.
InterPro; IPR001800; Lipoprotein_6.
                                                                                                                                                                                                                                                                                                                                                  191
                                                                                                                                                                                                                                                                                                                                                                             171
                                                                                                                                                                                                                                                                                                                                                                                                        131
                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: STRONG, TO VMP24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSCNNGGPE-----LKSDEVAKSDGTVLDLAKISKKIKDASDFAASVKEVHTLVKSIDEL
                                                                                                                                                                                                                                                                                                                                                  ANDAVETVIKELTASVKAEKPSQ
                                                                                                                                                                                                                                                                                                                                                                AKEMLANSVKELTSPVVAESPKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAKAIGKKI-HQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLK----NEGLKEKIDA
                                                                                                                                                                                                                                                                                                                                                                                                        VKKESEAFVTQVKSKHTDLAKEGVTDAHAKSAILVTDGTKDKGAAELIKLNTAIDELLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -AKAIGKKIKNDNSNFEDENDHNGSLIAGVFQVILTVKAKLTSLEQIIGISDELKTEVGM
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92; Conserv
FILAMENTS.
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215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
215
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23139
HEXAMER OF 2 HEAVY CHAIN SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 397; DB 1;
Pred. No. 3.4e-12;
5; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIABLE MAJOR OUTER MEMBRANE LIFOPROTEIN 3. N-ACYL DIGLYCERIDE (PROBABLE); 684C74D35F87C771 CRC64;
                                                                                                                                                                                                                                                                                                                                                  213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROBABLE
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                              1509
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               TWO-HEADED.
                                                                                                                                                                                                                     update)
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                                        BINDS
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                                        TO F-ACTIN
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              IT SELF-ASSEMBLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                  evidence
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(MHC),
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                                         HAS
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                                                                                of of
ALKALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                    170
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Best Local
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InterPro; IPR001609; myosin_head.
Pfam; PF00612; IQ; 2.
Pfam; PF00013; myosin_head; 1.
PFINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00012; MYSG; 1.
                                                                                                                                                                                                                                                                                                                          MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
SEQUENCE
                                        187
                                                                                                                                                                                                                                                                                                                                                                                                                                          NP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAKI, SHOULE, 1.

PROSITE; PS50096; IQ; 1.

Myosin; Coiled coil; Actin-binding; ATP-binding; Calmodulin-binding; Methylation; Alkylation; Phosphorylation; Multigene family.

MYOSIN HEAD-LIKE.
                                                                                                    138
                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                991
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y00624; CAA68663.1; -. PIR; A27224; A27224. HSSP; P08799; IMND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                          934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                      28
KSKLSAAEKSLKTAKDQNRDLDEQLEDERTYRANYDKQKKALEAKLTELEDQYTALDGQK 1166
                                                         DDVTATKLQLEKTKKSLEEELAQTRAQLEE-EKSGKEAASSKAKQLGQQLEDARSEVDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MLC-2).

(MLC-2).

(MLC-2).

(MLC-2).

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(MLC-2).

(MLC-2).

(MLC-2).

(MLC-2).

(MLC-2).

(A HEPTAPEPTIDES CYCLES OF 4 HEPTAPEPTIDES CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES CHARACTERISTIC OF ALCHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NONHELICAL TAILPIBECE WHERE THE REGULATORY PHOSPHORYLATION SITES RESIDE MISCELLANEOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTIVITY.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 2 IQ DOMAINS.
                            ----VAESPKKPSMVNNSG-----KDGNTSANSADESVKG--PNLTEISKKIT---
                                                                                     -DAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPV------
                                                                                                                   YEDEAAAHDSLKKKEEDLSRE-LRETKDALADAENISETLRSKL--KNTERGADDVRNEL
                                                                                                                                    ELQEETSASNDILEQKRKLEAEKGELKASLEE---EERNRKALQEAKTKVESERNELQDK 990
                                                                                                                                                                                                         EINKKITDSNAVLLAVKEVEA----LLSSIDEIAAKAIGKKIHO--NNGLDTENNHNGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIGHT CHAIN
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1483
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                                                                                                    819
1509
1226
1252
1509
1482
1509
1489
189
682
780
133
700
                                                                                                                                                                                                                                                             9.4%;
24.7%;
                                                                                                                                                                                                                                                                                                                        171201
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                                                                                                                                                                                                                                          Pred. No. 0.38
3; Mismatches
                                                                                                                                                                                                                                                           Score 174.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
PHOSPHORYLATION.
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IQ.
COILED COIL (POTENTIAL).
ALPHA-HELICAL TAILPIECE
                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                           ACTIN-BINDING. ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NONHELICAL TAILPIECE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALPHA-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIGHT MEROMYOSIN (LMM)
                                                                                                                                                                                                                                                                                                                  2CE49BE51173D17E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 REGULATORY LIGHT CHAIN SUBUNITS
                                                                                                                                                                                                                                                           .38;
                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                          159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAILPIECE (LMM)
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                      Length 1509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (S2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL outstation
                                                                                                                                                                                                                                          67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration
                               -ES
                                                                                                                                                                                                                                        Gaps
                                                            1106
                                                                                                                     1047
                             230
                                                                                         186
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RESULT

HISTORY

HIST
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                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, C
01-FEB-1991 (Rel. 17, L
15-JUL-1999 (Rel. 38, L
M PROTEIN, SEROTYPE 5 P
                                                                                         Transmembrane;
                                                                                                                                                                                   Pfam; PF00746; Gram_pos_anchor; Pfam; PF02370; M; 9.
                                                                                                                                                                                                                                     InterPro; IPR001899; Gram_pos_anchor
InterPro; IPR003345; M_repeat.
                                                                                                                                                                                                                                                                                            PIR; A03501; MMSOMP. PIR; A28616; A28616.
                                                                                                                 Virulence;
                                                                                                                                              PROSITE;
                                                                                                                                                                PRINTS; PR00015; GPOSANCHOR
                                                                                                                                                                                                                                                                                                                                         EMBL; M20374; AAA26976.1;
                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miller L., Gray L., Beachey E., Kehoe M.;
"Antigenic variation among group A streptococcal M proteins.
"Nucleotide sequence of the serotype 5 M protein gene and its
relationship with genes encoding types 6 and 24 M proteins."
J. Biol. Chem. 263:5668-5673(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      streptococci.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 43-212 AND 238-250.
MEDLINE=84162039; PubMed=6368549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M5_STRPY P02977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manjula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197-residue fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMM5 OR SMP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1278 -- AEKNLDKANLELEELRQEADDAARDNDKLVKDNRK 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE BACTERIUM AND CAN RENDER THE ORGAN
PHAGOCYTOSIS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE
SUBLARITY: TO OTHER M PROTEINS.
SIMILARITY: TO OTHER STREPTOCOCCAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ptococci.;

stol. Chem. 259:3686-3693(1984).

FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SERO OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE OF PROTEIN M. PROTEIN M RENDER THE ORGANISM RESISTANT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ula B.N., Acharya A.S., Mische S.M., Fairwell T., Fischetti complete amino acid sequence of a biologically active residue fragment of M protein isolated from type 5 group A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAVVLAVKEIETLLASIDELATKAIGKKIQQNGGLA--VEAGHNGTLLAGAYTISKLITQ
                                                                                                                                        PS00343;
                                                                                      S00343; GRAM_POS_ANCHORING; Phagocytosis; Cell wall; Dane; Coiled coil; Signal.
                     43
43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO OTHER M PROTEINS.
TO OTHER STREPTOCOCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=3281944;
, Beachey E., Kehoe M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence up Last annotation PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
M PROTEIN, SEROTYPE 5.
EXTRACELLULAR (POTENTIAL).
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                                                                                                 Duplication; Repeat;
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                                                                                                      Antigen;
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                                                                                           BAG_STRAG STANDARD; PRT; 1164 AA. P27951; O1-AUG-1992 (Rel. 23, Created) O1-AUG-1992 (Rel. 23, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B A
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REPEAT
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                                             Streptococcus.
NCBI_TaxID=1311;
                                                                 Streptococcus agalactiae
Bacteria; Firmicutes; Bac
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          MEDLINE-91312121; PubMed-1857207;
                             SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                             LKE----KIENAKKCSE
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                                                                                                                                                                                                                                                                                                                                                      ---KIAKEQENKETI-----GTLKKILDETVKDKIAKEQENKET
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Similarity 24.9%;
07; Conservative 5
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                              AND
                                                                   Bacillus/Clostridium group; Streptococcaceae;
                             SEQUENCE
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Pred.
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CYTOPLASMIC (POTENTIAL).
GLY/PRO-RICH (CELL WALL-SPANNING)
CONSERVED IN GRAM-POSITIVE COCCI:
PROTEINS.
5 x 7 AA TANDEM REPEATS OF L-K-T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A -> T (IN REF. 2).

N -> S (IN REF. 2).

K -> SNLERKTAELTSEK (IN REF. 2).

1 -> L (IN REF. 2).

873779B6CBD55E27 CRC64;
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 Timmis K.N.
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                                                                                                                                                                                                                                                                                             -DFTKKLEGEHAQLGIENVTDENAKKAI-L
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.14;
                                                                                              (B ANTIGEN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The IgA-binding beta antigen of the streptococci: sequence determination
                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00746; Gram_pos_anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001899; Gram_pos_anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S15330; FCSOAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X59771; CAA42442.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97035265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Microbiol. 5:843-849(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding
                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin
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378
                   289
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                                                                                                                                       KEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL
                                                                                                                                                                     TKVDLSN-IDKELNHQKS-
                                                                                                                                                                                  KKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL
                                                                                                                                                                                                                        SGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVK---EVEALLSSIDEIAAKAIG
KLNQSKNLPELKQLEEEAHSKLKQVVEDFRKKFKTS-----
                  KLDGLKNSEKLKEKIENA----KKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAA
                                                                                  DQEIQEHVKKETSSEENTQKVDEHYANSL-QNLAQKSLEELDKATTNEQATQVKNQFLEN
                                                                                             LKKIEDIRKQ-AQQADKKE-----DAEVKVREELGKLFSS----TKAG------L
                                                                                                                                                                                                             SHEQKNEFKTKIDETNDSDALLELENQFNETNR-LLHIKQHEEVEKDKKAKQQKTLKQSD
                                        AQKLKEIQPLIKETNVKLYKAMSESLEQ----VEKELKHNSEANLEDLVAKSKEIVREYEG
                                                            --AVKEIETLLASIDELATKAIGKKIQQNGGLAVEAGHNG----TLLAGAYTISKLITQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00409;
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                                                                                                                                                                                                                                                                Score 164.5;
Pred. No. 0.8
                                                                                                                                                                                                                                                                                                                              IG-LIKE DOMAIN.
IG-BINDING (POTENTIAL).
IGA-BINDING (POTENTIAL).
PRO-RICH REPEATS.
CONSERVED IN GRAM-POSITIVE
                                                                                                                                                                                                                                                                                                                                                                                 IGA FC RECEPTOR.

EXTRACELLULAR (POTENTIAL).

MEMBRANE ANCHOR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                      PROTEINS
                                                                                                                                                                                                                                                       Mismatches
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 -EQVTPKKRVKRDL---
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RESULT
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ID USO1_YEAST
P25386;
P25387
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CONFLICT
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                                                                                               DOMAIN
                                                                                                           DOMAIN
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                                                                                                                       DOMAIN
                                                                                                                                      DOMAIN
                                                                                                                                                              InterPro;
                                                                                                                                                                                                         PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bai Y., Symington L.S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER TO THE GOLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=X2180-1A;
MEDLINE=91185402; PubMed=2010462;
MEDLINE=91185402; PubMed=2010462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-8 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kendrick K.E.;
Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 782-1790 FROM N.A.
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01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.
USO1 OR INT1 OR YDL058W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hostetter M.K., Herman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales; Saccharomycetaceae; NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakajima H., Hirata A., Yamasaki M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast)
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A cytoskeleton-related gene, usol,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              429
                                                                                                                                                                                                                                                                                                                                                          MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.

ER AND THE GOLGI COMPLEX.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.

SIMILARITY: BELONGS TO THE VDP/USOL/YBL047C FAMILY.
                                                                                                                                                           ", P80220; 1DIP.
S0002216; USO1.
rPro; IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                otein transport in Saccharomyces Cell Biol. 113:245-260(1991).
                                                                                                                                                                                                  A38455; A38455.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NENNQOKIE-LTVSPENI 445
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1253
1319
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                                                                                                                                             transport;
                                                                                                                                                        Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.J.,
GLOBULAR HEAD.

COLLED COLL (POTENTIAL).
CHARGED (HYPER-HYDROPHILIC).
CHARGED (HYPER-HYDROPHILIC).
DISPENSABLE FOR THE PROTEIN FU
ASP/GLU-RICH (ACIDIC).
G -> E (IN REF. 2).
E -> K (IN REF. 2).
V -> I (IN REF. 2).
I -> V (IN REF. 2).
N -> S (IN REF. 2).
                                                                                                                                Golgi stack; Cytoskeleton; Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bendel C.M., McClellan M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yonehara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , is required cerevisiae.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetes;
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                      342 DAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL
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SEQUENCE
                                                                           282
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                                                                                                                                                                                                                                                                                        985
                                                                                                                                                                                                                                                                                                                                      929
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                                                                                                                                                                                                                                                                                                               53
                                                                                                                                                                                                                                                                                                                                                3 CNNSGKDG------NTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSS
--AKEKSESELSRLKKTSSEERKNAEEQLEKLKNEI 1358
                                                                                        IDALNLOIKELKKKNETNEASLLESIKSVESETV--KIKE---LQDECNFK------
                                                                                                                                                                                 LETSEKALKEVKENEEHLKEEKIQLEKEATETKOQLNSLRANLESLEKEHEDLAAQLKKY 1164
                                         -EKEVSELEDKLKASEDKNSKYLELQKESEKIKEELDAKTTELKIQLEKITNLSK-----
                                                              ISKLITOKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILIT
                                                                                                            SNAVVLAVKEIE-----TLLASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYT
                                                                                                                                    EEQIANKERQYNEEISQLNDEITSTQQENESIKKKNDELEGEVKAMKSTSEEQSNLKKSE 1224
                                                                                                                                                         KEMLANSVKELTSPV--VAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITE 229
                                                                                                                                                                                                                 ADAKEAILK---
                                                                                                                                                                                                                             SDSSKDEYESQISLLKEKLETATTANDENVNKISELTKTREELEAELAAYKNLKNELETK 1104
                                                                                                                                                                                                                                                         LDGLKNEG-----LKEKIDAAKKCSETFTNKLKE---
                                                                                                                                                                                                                                                                            VEESKNESSIQLSNLQNKIDSMSQEKENFQIERGSIEKNIEQLKKTISDLEQTKEEIISK
                                                                                                                                                                                                                                                                                                 IDEIAAKAIGKKIHQNNGLD--TENNHNGSLLAGAY------AISTL----IKQK
                                                                                                                                                                                                                                                                                                                         CNNLSKEKEHISKELVEYKSRFQSHDNLV--AKLTEKLKSLANNYKDMQA--ENESLIKA 984
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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1600
1661
1772
1790
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1600
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                                                                                                                                                                                                                                                                                                                                                                                           .78;
                                                                                                                                                                                                                                                                                                                                                                             72;
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DRHG
                                                                                                                                                                                                                                                                                                                                                                                        Score 161.5;
Pred. No. 1.
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-> V (IN RE

-> S (IN RE

-> DEEDDEE
                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   -> S (IN REF. 2).
-> V (IN REF. 2).
-> S (IN REF. 2).
-> DEEDDEE (IN REF.
6CE2B216E9FD4818
                       377
                                                                                                                                                                                                                                                                                                                                                                                       .8;
                                                                                                                                                                                                                                                                                                                                                                          178;
                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                     ----KHTDLGKEGVTD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                         Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                1790;
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                      1270
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REST
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Griparic L., Keller T.C. III;

"Identification and expression of two novel CLIP-170/Res
expressed predominantly in muscle.",
submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SEEMS TO BE A INTERNEDIATE FILAMENT ASSOCITHAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES (BY S)
                                                                                                                                                                                                                                                                                                                  REST_CHICK STANDARD,
042184: 042228: 057563: 057564;
057563: 057564;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                   TISSUE=Pectoralis muscle;
                                                                                                                 SEQUENCE OF 17-1139 FROM N.A.
                                                                                                                                                   Griparic L., Volosky J.M., "Cloning and expression of Gene 206:195-208(1998).
                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=98137792; PubMed=9469933;
                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHICK
                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                   Archosauria;
                                                                                                                                                                                                                                                                                     Aves;
                                                                                                                                                                                                                                                                                Neognathae;
                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                 Keller T.C.
chicken CLI
                                                                                                                 (CLIP-170(11) AND
                                                      two novel CLIP-170/Restin
                                                                                                                                                                 T.C. III;
CLIP-170
                                                                                                                                                                 and
                                                                                                           CLIP-170(11+35)).
                                                                                                                                                               restin
                 ASSOCIATED PROTEIN
   (BY SIMILARITY)
                                                                                                                                                             isoforms.";
                                                                                                                                                                                                                                                                         Phasianinae;
                                                               isoforms
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Query Match
Best Local
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EMBL; AP020764; AAC60345.1; -.
EMBL; AP045650; AAC03547.1; -.
EMBL; AF045651; AAC03548.1; -.
InterPro; IPR000938; CAP-Gly.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF01302; CAP_GLY; 2.
SMART; SM00343; Znf_C2HC; 1.
PROSITE; PS00845; CAP_GLY_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
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ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS ARE PRODUCED ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY:
                                                                                                                                       KAIGKKIQQNGGLAVEAGHNGTL----LAGAYTISKLITQKL-DGLKNSEKLKEKIENAK
                                                                                                                                                                                                                                                                                                                                                   EINKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHQNNGLDTENNHNGSLLAGAYA
                                                                                                                                                                                                                                     KPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELAT
                                                                                                                                                                                                                                                                            GVGAQTAEFAELKTQMEKVKLDYE--NEMSNLKLKQENEKSQHLKEIEALKAKLLEVTEE
                                                                                                                                                                                                                                                                                                               GVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVVAESPK
NLAKAAKEML 370
                                                                                                                KLIGSLTQQ-----IRASEEKLLDLAALQKANSEGKLEIQKLSEQLQAAEKQIQNLETEK
                                                                                                                                                                                                KEQTLEN-----LKAKLESVEDQHLVEMEDTLNKLQEAEIKVKELDVLQAKCNE-QT
                                                                                                                                                                                                                                                                                                                                                                                            ISTL-IKQKLDGLKNEGLKEKIDAAKK----CSETFTNKLKE---KHTDLGKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                   ESSKHIDDVDTSLSLLQEI----SSLQEKMA-AAGKE-HQREMSSLKEKFESSEEALRKE
                                                                           KCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAEL---
                                      --VSNLTKELQGKEQKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1414
458
458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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207
277
332
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1427
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25.9%;
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CCHC-BOX.

MISSING (IN SHORT ISOFORM).

TOTKLEHARIKELEQSLLFEKTKADKLQRELEDTR ->
RKRQISEDPEN (IN ISOFORM CLIP-170(11)).

S -> GGSKVS (IN ISOFORM CLIP-170(11)).

T -> RKRQISEDPENT (IN ISOFORM CLIP-
170(11+35)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coiled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 160;
Pred. No. 1
                                      LDLEKNLSAVNQVKDSLEKELQLLKEKFTSAVDGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SER-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAP-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> R (IN REF. 2; AAC03547).
-> V (IN REF. 2; AAC03548).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5631CE8683498E23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                           -EKLFKAV---E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
                                                                                                                                                       307
                                                                                                                                                                                                                                                                            695
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В

S

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RX MEDLING-20196006; PubMed-10731132;
RX Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer E.G., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Baxen B. P., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler R.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Geodson K., Doup L.E., Downes M., Dugan Rocha S., Pleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Glu Z., Glabar W. M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Patches J.M.,
Ra Nanara Y., Venesse M., Supper M., Skupski M.P., Shen H.,
Ra Shen B.C., Siden-Riamos I., Simpson M., Skupski M.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JLT 10
L_DROME
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p15215; Q24373; Q9V9118;
O1-APR-1990 (Rel. 14, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LAMININ GAMMA-1 CHAIN PRECURSOR (LAMININ B2 CHAIN).
LANB2 OR LAMC1 OR LAMG1 OR CG3322.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CANTON-S, AND OREGON-R;
MEDLINE-91299161; PubMed-1840513;
Chi H.-C., Juminaga D., Wang S.Y.,
"Structure of the Drosophila gene
DNA Cell Biol. 10:451-466(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chi H.-C., Hui C.-F.;
"Primary Structer of the Drosophila laminin B2 chain and comparison with human, mouse, and Drosophila laminin B1 and B2 chains.";
J. Biol. Chem. 264:1543-1550(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Montell D.J., Goodman C.S.;
"Drosophila laminin: sequence of B2 su
three subunits during embryogenesis.";
J. Cell Biol. 109:2441-2453(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Spradling A.C., Stapieton .... Venter E., Wang A.n., .... R., Tector C., Turner R., Venter E., Wang A.n., .... .... Yeissenbach J.,
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InterPro; IPRO0004; Laminin_B.
InterPro; IPRO02049; Laminin_BGF.
InterPro; IPRO02049; Laminin_BGF.
Pfam; PF00052; laminin_BGF; 1.
Pfam; PF00053; laminin_RGF; 1.
Pfam; PF00055; laminin_Nterm; 1.
ProDom; PD002082; LamNT; 1.
ProDom; PD002081; LamNT; 1.
ProDom; PD003031; Laminin_B; 1.
SMART; SM00180; EGF_Lam; 10.
SMART; SM00018; LamB; 1.
SMART; SM00018; LamB; 1.
SMART; SM000186; LamNT; 1.
SMART; SM00136; LamB; 1.
                                                                                                                                                                                                                                                                                                SMART; SM00281; LamB; 1.
SMART; SM00136; LamNT; 1.
PROSITE; PS00022; EGF 1; 8.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; LANININ TYPE EGF; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CDNA and amino acid sequences of Drosophila laminin B2 chain.";
Nucleic Acids Res. 16:7205-7205(1988).

-i FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING EMBRYONIC DEVELOPMENT BY INTERACTING OF THREE TO THE EXTRACELLULAR MATRIX COMPONENTS.

-i SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE TO EACH OTHER BY DISULTED BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THEE SHORT ARMS WITH GLOBULES AT EACH END.

-i SUBCELLULAR LOCATION: BASEMENT MEMBRANES (MAJOR COMPONENT).

-i DOMAIN: THE ALPHA HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT DOMAIN: THE ALPHA HELICAL DOMAINS I AND IT ARE THOUGHT TO INTERACT SIMILARITY: CONTAINS I LAMININ GLOBULAR.

-i SIMILARITY: CONTAINS 1 LAMININ STENDED MOMAINS.

-i SIMILARITY: CONTAINS 1 LAMININ PETERMINAL DOMAIN (DOMAIN VI).

-i SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M58417; AAA28665.1; --
EMBL; M25063; AAA28664.1; --
EMBL; AE003551; AAF50238.1; --
EMBL; X07806; CAA33665.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0002528;
InterPro; IPR000561; E
InterPro; IPR001886; I
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MEDLINE=8303364; PubMed=3405777;
Chi H.-C., Hui C.-F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Smith Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                   EGF-like domain;
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                                 LAMININ GAMMA-1 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (IV).
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (N-TERMINAL).
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nesion; Repeat; Signal.
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N EGF-LIKE 2.
N EGF-LIKE 4.
N EGF-LIKE 4.
N EGF-LIKE 5 (N-TERMINAL).
N DOMAIN IV.
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                                          ETFTNKLK-EKHTDLGKEGVTDADAKEAILKAN-------
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COOLLED COIL (POTENTIAL
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Pred. No. 2;
3; Mismatches 162;
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VIN EGF-LIKE 10.

VIN EGF-LIKE 11.

VIN EGF-LIKE
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Hypothetical
SEQUENCE 19
                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                 Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Schizosaccharomyces.
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L 222.8 KDA PROTEIN C1F3.06C IN CH
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                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1957
                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHROMOSOME
                                                                                                                                                                                                 151;
                                                                                                                                                                                                                            Length 1957;
                                                                                                                                                                                                 Indels
                                                                                                                    -----NHNGSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                        M.A.,
                                                                                                                                                                                                                                                                                                                                                                         restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                        Walsh
                                                                                                                                                                                                 141;
                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                        S.V.;
                                                                                                                    82
                                                                                                                                               418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRPY
            PRINTS; PRO0015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING;
Virulence; Phagocytosis; Cell wall; Du
Transmembrane; Coiled coil; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINB-#86111835; PubMed-3511046;

Hollingshead S.K., Fischetti V.F., Scott J.R.;

Micomplete nucleotide sequence of type 6 M protein streptococcus. Repetitive structure and membrane a J. Biol. Chem. 261:1677-1686(1986).
                                                                Pfam; PF00746; Gram_pos_anchor; Pfam; PF02370; M; 9.
                                                                                         InterPro; IPR001899; Gram_pos_anchor
InterPro; IPR003345; M_repeat
                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1988
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P08089;
                                                                                                                      PIR; A26297;
                                                                                                                                 EMBL; M11338; AAA26920.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 43-122 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: TYPE I MEMBRANE SIMILARITY: TO OTHER M PROTEINS. SIMILARITY: TO OTHER STREPTOCOCCAL AND IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                        PHAGOCYTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNELKGELQTEISNSEHLSSQLSTLAAEKEAAVATN-----NELSESKNSLQTLCNAF
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Last annotation
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                          Duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Scott J.R., Pulliam W.M., Hollingshead S.K., Fischetti V.A.;
Scott J.R., Pulliam W.M., Hollingshead S.K., Fischetti V.A.;
"Relationship of M protein genes in group A streptococci.";
Proc. Natl. Acad. Sci. U.S.A. 82:1822-1826(1985).
-1- FUNCTION: THIS PROTEIN MIS CLOSELY ASSOCIATED WITH VIRULENCE OF PROTEIN M. PROTEIN MIS CLOSELY ASSOCIATED WITH VIRULENCE THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKNTNAILSSELT--KSSEDVKRLTANVETLTQDSKAMKQSFTSLVNSYQSI
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Repeat; Antigen;
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MYSN_DROME

ID MYSN_DROME

AC 099323;
DT 01-JUN-1994
DT 20-AUG-2001
DE MYOSIN HEAVY
GN ZIP.
OC Pterygota; N
OC
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Ketchum A.S., Stewart C.T., Stewart M., Kiehart D.P.;
"Complete sequence of the Drosophila nonmuscle myosin h
transcript: conserved sequences in the myosin tail and
splicing in the 5' untranslated sequence."
Proc. Natl. Acad. Sci. U.S.A. 87:6316-6320(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                        01-JUN-1994
01-JUN-1994
20-AUG-2001
                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atches
                                                                                                                                                     TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seguence update)
20-AUG-2001 (Rel. 40, Last annotation updat
MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROT
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                       NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367
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                CELLULARIZATION.
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92; Conserv
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        REQUIRED FOR MORPHOGENESIS AND
                                                                                                                                                                                                                                                                                                 NON-MUSCLE
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23.0%;
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                          MYOSIN APPEARS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64;
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TWO DIRECTLY REPEATED 27 AMINO ACID
BLOCKS SEPARATED BY 15 AMINO ACIDS.
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CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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10 X 7 AA TANDEM REPEATS.
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                                                                    nonmuscle myosin heavy-chain
he myosin tail and differential
                                                                                                                                                                                                                                                                                                                                                                                 2017
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                     BE RESPONSIBLE FOR
                                                                                                                                                                                                                   Hexapoda; Insecta;
a; Brachycera; Muscomorpha;
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       CYTOKINESIS
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Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00015; IQ; 1.
DB0677777 ST000042; MYSC; 1.
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InterPro; IPR000048; IQ.
InterPro; IPR00128; Myosin_tail.
InterPro; IPR001609; myosin_head.
Pfam; PF00611; IQ; II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding;
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PIR; B36014; B36014.
HSSP; P08799; 1MND.
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It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as its content is in no way that it is a subject to the state of the swing as its content is in no way that it is the swing as its content is in no way that it is the swing as its content is in no way that it is the swing as its content is in no way that it is the swing as its content is in no way that it is the swing as its content is in no way that it is the swing as its content is in no way that it is the swing as its content is in no way that it is the swing as its content is in no way that it is in the swing as its content is in no way that is the swing as its content is in no way that is the swing as its content is in no way that is the swing as its content is in no way that is the swing as its content is in no way that is swing as its content is in no way that is still not a swing as its content is in no way that is swing as its content is in no way that is still not a swing as its content is in no way that is still not say that it is still not say that is still not say that it                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M35012; AAA28713.1; -.
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SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                            QQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEK----IENAKKCSEDFTK
                                                                                                                                                                                                                                                   KRLNK----DIEALERQVKELIAQNDRLDKSKKKIQSELEDATIELEAQRTKVLELEKKQK
                                                                                                                                                                                   NTSANSADESVKGPNLTE----ISKKITESNAVVLAV-KEIETLLASIDELATKAIGKKI 259
                                                                                                                         NFDKILAEEKAISEQIAQERDTAEREAREKETKVLSVSRELDEAFDKIEDLENK----RKT 1552
                                                                                                                                                                                                                                                                                                                EELGKLFESVEVLSKAAKEMLANSVK------ELTSPVVAESPKKPSMVNNSGKDG
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Pred. No. 5.
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MW; 73E3CB02BA8F2528
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ALPHA-HELICAL TAILDIECE (LMM).
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528 CRC64;
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, outstation -
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RESULT 14

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                                                                                                                                                           HOUGUSSE A., Cohen C.;

"Structure of the regulatory domain of scallop myosin at 2-A

"Structure of the regulations for regulation.";

RT resolution: implications for regulation.";

RT resolution: implications for regulation.";

RT resolution: MUSCLE CONTRACTION.

C:- FUNCTION: MUSCLE CONTRACTION.

C:- FUNCTION: MUSCLE CONTRACTION.

C:- FUNCTION: MUSCLE MYOSIN IS A PROPER THAT BINDS TO F-ACTIN & HAS ATPASE

C:- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C:- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C:- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIS (MIC-2).

C:- SUBURIT: MUSCLE MYOSIN TIS A HEXAMENIS (MIC-2).

C:- SUBURIT: MUSCLE MYOSIN SUBURITS (MIC-2).

C:- SUBURIT: MUSCLE MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

C:- SIMILARITY: CONTAINS 1 IQ DOMAIN.
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P24733;
                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-MAR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN, STRIATED MUSCLE.
Aequipecten irradians (Bay Scallop).
Eukaryota, Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
Pectinoidea; Pectinidae; Argopecten.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nyitray L., Goodwin E.B., Szent-Gyorg "Nucleotide sequence of full length c muscle myosin heavy chain.";
Nucleic Acids Res. 18:7158-7158(1990)
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"Complete primary structure of a scallop striated muscle myosin heavy chain. Sequence comparison with other heavy chains reveals regions that might be critical for regulation.";
13. Biol. Chem. 266:18469-18476(1991).
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MEDLINE-92011595; PubMed-1917970;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:306-312(1994).
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X55714; CAA39247.1;
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Best Local Similarity
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
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PDB; 1WDC; 11-JUL-96.
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PIR; A40997; A40997
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                       324 LGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVEN
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                                                                                                                                                                                                                                                                                          925
                                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                         18 DESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHQNNGLDT----
                                                                                                                    DELATKAIGKKIQQNGG-------LAVEAGHNGTLLAGAYTISKL-----
                                                                                                                                            EAEISSLNSKLEDEQNLVSQLQRKIKELQARIEELEEELEAERNARAKVEKQRAELNREL
                                                                                                                                                        PKKPSMVNNSGKDGNTSANSADESVK--GPNLTEISKKI-TESNAVVLAVKEIETLLASI : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                   KEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVVAES
                                                                                                                                                                                                                                            ISQQDEHIGKLNKEKKALEEANKKTSDSLQAE - - EDKCNHLNKLKAKLEQALDELEDNLE
                                                                                                                                                                                                                                                                  ---ENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKEKHTDLG
                                                                                                                                                                                                                                                                                       DEEDAAADLEGIKKKMEADNA-----NLKKDIGDLENTLQKAEQDKAHKDNQISTLQGE 978
L---NARLEDSQRSINELQSQKSRLQAENSDLTRQLED 1290
                                               AANEMADQVDQLQKVKSKLEKDKKDLKREMDDLESQMTHNMKNKGCSEKVMKQFESQMSD
                                                                     - ITOKLDGLKNSEKLKEKIENAKK--
                                                                                             EEL-----GERLDEAGGATSAQIELNKKREAELLKIRRDLEEASLQHEAQISALRKKHQD
                                                                                                                                                                                           REKKVRGDVEKA-----KRKVEQDLKSTQENVEDLERVKRELEEN-----
                                                                                                                                                                                                                                                                                                                                        81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00015; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                   8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myosin_head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                                                                   Score 150; DB Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COILED COIL (POTENTIAL).
ATP (BY SIMILARITY).
ALKYLATION (SH-1) (BY SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALKYLATION (SH-1)
ALKYLATION (SH-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RODLIKE TAIL (S2 AND LMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 A5CCE4127D1A4896 CRC64
                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                        166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                             Length 1938;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                      -CSEDFTKKLEGEHAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAINS)
                                                                                                                                                                                                                                                                                                                                        66;
                                                                                                                                                                                            -VRRK
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                    247
                                                                                                                                                                                                                    190
                                                                                                                                                                                                                                            1036
                                                                                                                                            1140
                                                                                                                                                                                            1080
                                                                                              1195
                                                                                                                                                                                                                                                                   130
                                                                                                                      285
                                                                                                                                                                                                                                                                                                                                        12;
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C -!- FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
C -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
C -!- SUBUNITS (MCC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
C -- ALKALI SUBUNITS (MCC), 2
C -- SUBCELULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
C -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
C CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
C -- CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.
C -- PTM: TWO CYSTEINE RESIDUES IN THE 51 DOMAIN ARE SELECTIVELY
C ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
C -- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
C SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                 Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                          SMART; SM00242; MYSC; 1.
MYOSIn; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J01050; AAA28124.1;
EMBL; V01494; CAA24738.1;
PIR; A02992; MWKW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83273600; PubMed=bɔ/ʊɔɔɜ,
MEDLINE-83273600; PubMed=bɔ/ʊɔɔɜ,
Karn J., Brenner S., Barnett L.;
"Protein structural domains in the Caenorhabditis elegans unc-54
"protein structural domains in the Caenorhabditis elegans unc-54
"proce Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
                                         DOMAIN
                                                                             DOMAIN
                                                                                                      DOMAIN
                                                                                                                                          DOMAIN
                                                                                                                                                             ATP-binding; Methylation;
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT.-1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1876-1966 FROM N.A. MEDLINE-83232892; Pubmed-6571695; Wills N. Gesteland R.F., Karn J., Waterston R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nonsense mutations via altered transfer Cell 33:575-583(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McLachlan A.D., Karn J.;

"Periodic charge distributions in the myosin rod amino acid sequence match cross-bridge spacings in muscle.";

Nature 299:226-231(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The genes \sup -7 \times \text{and } \sup -5 \text{ III of C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 850-1966 FROM N.A. MEDLINE-82272395; PubMed-72021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Rhabditidae; Pelode:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNC-54 OR MYO-4.
Caenorhabditis elegans.
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851
1165
1165
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         850
1966
1164
1176
1176
                                                                                                                                                                                                                                                       myosin_head; 1.
                                                                                                                                                   Alkylation; Multigene family.
HINGE.
LIGHT MEROMYOSIN (LMM)
                                                                                                MYOSIN HEAD-LIKE
COILED COIL (POT)
                                                         ALPHA-HELICAL TAILPIECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barnett L., Bolten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elegans suppress amber
r RNA.";
                                                                                                (POTENTIAL)
                                                                (S2).
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Best Local
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DOMAIN
DOMAIN
MOD_RES
MOD_RES
MOD_RES
CONFLICT
CONFLICT
SEQUENCE
                                                                         284
                                                                                                                                                              186 VVAESPKKPSMVNNSGKDGNTSANSADESVKGPNL--TEISKKITESNAVVLAVKEIETL
                                                                                                                       244
                                                                                                                                                                                                                   129
                                                                                                                                                                                                                                                                                                       16 SADESVKGPNLTEINKKITDSNAVLLAVK---EVEALLSSIDEI--AAKAIGKKIHQ-NN 69
                                                                                                                                                                                                                                                                70
EQRNGADTREQFFNAEKRATLLQSEKEELLVANEAAE
                                                                                          RAQVEVSQIRSEIEKRIQEKEEEFENTRKNHARALESMQASLETEAKGKAELLR-----
                      AKDKGAAELEKLFKAVE--NLAKAAKE--MLANSVKE
                                                                   KLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDA
                                                                                                                                                                                                             LGKEGVTDADAKEAILKANGT---KTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSP 185
                                                                                                                                                                                                                                   ALDAANSKNASLEKTKSRLVGDLDDAQVDVERANGVASALEKKQKGFDKIIDEWRKKTDD 1474
                                                                                                                                                                                                                                                                                 SLEEEIEGKN--EILRQLSKANADIQQWKARFEGEGLLKA-DELEDAKRRQAQKINELQE 1414
                                                 -- IKKKLEG
                                                                                                                      LASIDELATKA-IGKKIQQ----
                                                                                                                                                                                       LAAE - - - - LDGAQRDLRNTSTDLFKAKNAQE - - ELAEVVEGLRRENKS - LSQEIKDLTDQ
                                                                                                                                                                                                                                                           GLDTENNHNGSL-LAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKEKHTD 128
                                                                                                                                                                                                                                                                                                                                      90;
                                                                                                                                                                                                                                                                                                                                   Similarity 22.
90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                177
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                                            --DINELEIALDHANKANADAQKNLKR-----YQEQVRELQLQVEE 1671
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687
783
128
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                                                                                                                                          ---GEGGRSVHEMOKIIRRLEIEKEELQHALDEAEA-ALEAEESKVL
                                                                                                                                                                                                                                                                                                                                                8.1%;
22.7%;
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                                                                                                                                                                                                                                                                                                                                  76;
                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                      METHYLATION (TRI-)
ALKYLATION (SH-1).
ALKYLATION (SH-2).
E > R (IN REF. 2).
I > L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                              Score 150;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (BY SIMILARITY).
ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                  -----NGGLAVEAGHNGTLLAGAYTIS
                                                                                                                                                                                                                                                                                                                                                                                             B66F0BB2FE27B67F
                                                                                                                                                                                                                                                                                                                                              .5;
                       376
                                                                                                                                                                                                                                                                                                                                  149;
                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                       Length 1966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                  82;
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                           1625
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Search completed: Job time: 967 sec March 18, 2002, 10:11:49

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SPTREMBL_17:*

Sp_archea:*

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sp_human:

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   protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                      Query
Match
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Gapop 10.0 , Gapext 0
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444.035 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
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664	664	664.5	664.5	664.5	664.5	666	666.5	666.5	667	670	675	681	683	683.5	685.5	686	686	686.5	690.5	692.5	696.5	707	709	739	773
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212	203	211	209	202	193	201	211	193	201	212	194	212	193	191	209	212	190	211	193	211	211	192	210	178	159
ν	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	2	N	N	N	N	N	N	2	2	N
Q44670	050624	Q49577	Q44883	P96508	P94233	P96573	Q9Z6C7	P94231	P96571	Q44727	P94247	Q44705	031115	P94245	Q44671	Q9KIM5	P94244	Q44976	P94242	Q49576	Q44977	Q9S3P2	Q44719	Q44994	Q9R7B0
borrelia	borrelia	borrelia	borrelia	P96508 borrelia af	borrelia	Q9kim5 borrelia af	borrelia	borrelia	borrelia	Q49576 borrelia af	borrelia	borrelia	borrelia		Q9r7b0 borrelia bu										

ALIGNMENTS

Qy 123 KEKHTDLGKEGVTDADAKEAILKANGTKTK	Qy 63 KKIHQNNGLDTENNHNGSLLAGAYAISTLI	Qy 3 CNNSGKDGNTSANSADESVKGPNLTEINKK	Query Match Best Local Similarity 99.0%; Pred. No. : Matches 190; Conservative 1; Mismatch	NON_TER 192 192 SEQUENCE 192 AA; 20287 MW;	DR ProDom; PD001149; Lipoprotein_6; 1. FT NON TER 1		Evidence for lateral transfer and	RN [1] RP SEQUENCE FROM N.A.			DE OUTER SURFACE PROTEIN C (FRAGMENT). GN OSPC.	13,	AC Q9S3P3; DT 01-MAY-2000 (TrEMBLrel, 13, Created)	RESULT 1 Q9S3P3 PRELIMINARY; PRT;	
KEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL 182	KKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL 122 	CNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKAIG 62 	Score 943; DB 2; Length 192; Pred. No. 2.6e-37; 1; Mismatches 1; Indels 0; Gaps 0;	. 11846F7AC84C7E3D CRC64;			Dorner F.; recombination in OspC variation in		caceae; Borrella.	spirochete).		Last sequence update) Last annotation update)		192 AA.	

Gaps

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182

122

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В
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P70818
ID P7
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Q9R7B1;
01-MAY-2000
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01-MAY-2000 (TIEMBLIEL. 13, Last sequence update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation update)
UTER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borreli
NCBI_TaxID-139;
                       U.S.A
                             MEDLINE=97478003; PubMed=9336916;
Ras N.M., Postic D., Foretz M., Baranton G.;
"Borrelia burgdorferi sensu stricto, a bacte
                                                                STRAIN-TETS
                                                                     SEQUENCE FROM N.A.
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STRAIN-2-1498 CA4;
Probert W.S., Crawford M.R.,
submitted (SEP-1996) to the I
EMBL; L81131; AAB06569 1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1. ProDom; PD001149; Lipoprotein_6; 1.
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NCBI_TaxID=139;
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           Syst.
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         Bacteriol.
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       47:1112-1117(1997).
                           M., Baran
stricto,
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Pred. No. 1.4e-36;
1; Mismatches 2
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Last annotation updat
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NON_TER
SEQUENCE
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                                                                                                                                                         InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                               EMBL; AF029860; AAB86543.1; -
                                                                                                                                                                                                 MEDLINE=99091544; PubMed=9872945;
Wang I.N. Dykhuizen D.E., Qiu W.,
"Genetic diversity of ospc in a loc
burgdorferi sensu stricto.";
                                                                                                                                                                                                                                                                                     Borrelia burgdorferi (Lyme Bacteria; Spirochaetales;
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01-JUN-2001
                                                                                                                                                   ProDom;
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NON_TER
NON_TER
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SEQUENCE FROM N.A.
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                   ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA
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                                                                          Similarity
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193
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l (TrEMBLrel. ]
ACE PROTEIN C
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(TremBLrel. 13, Last sequence update)
(TremBLrel. 17, Last annotation updat
CE PROTEIN C (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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97.9%;
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                                                                                                                   MW;
                                                                                                                                                                                                                                                                                     Spirochaetaceae;
                                                          Score 908; DB Pred. No. 1.1e. 3; Mismatches
                                                                                                                                                                                                                                                                                              disease spirochete).
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Pred.
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                                                               908; PE ...
No. 1.1e-35;
                                                                                                                                                                                                            Dunn J.J., Bosler E.M., L cal population of Borrelia
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No. 2.
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.7e-36;
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J databases.
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Matches 180
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01-MAY-2000
01-JUN-2001
O9R7B2 PRELIMINARY; PRT; 182 AA. 09R7B2; O1-MAY-2000 (TrEMBLrel. 13, Created) O1-MAY-2000 (TrEMBLrel. 13, Last sequence update O1-JUN-2001 (TrEMBLrel. 17, Last annotation update OUTER SURFACE PROTEIN C (FRAGMENT).

Borrelia burgdorferi (Lyme disease spirochaete).
Bacteria; Spirochaetales; Spirochaetaceae; Borre
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Plasmid.
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Bacteria; Spirochaetales;
NCBI_TaxID=139;
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CE PROTEIN C PRECURSOR (FRAGMENT).
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182 AA;
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Marti-Ras N., Postic D., Foretz M., Submitted (MAR-1997) to the EMBL/Ge EMBL, U91797; ABB81894.1; ... InterPro; IPRO01800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1.
                                            InterPro; IPR001800; Lipoprotein_6
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1
                                                                                              Livey I., Gibbs C.P., Schuster R., "Evidence for lateral transfer and Lyme disease Borrelia.", Mol. Microbiol 18:257-269(1995).
EMBL; L42895; AAB37003.1; -...
                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Created 01-MAY-1997 (TrEMBLrel. 03, Last see 01-JUN-2001 (TrEMBLrel. 17, Last an OUTER SURFACE PROTEIN C (FRAGMENT).
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                                                                                                                                                                                                                                                                                  Borrelia burgdorferi (Lyme
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Best Local
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                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
01-JUN-2001 (TREMBLREL. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
NON_TER
SEQUENCE
     Bacteria; Spirochaetales;
NCBI_TaxID=139;
                     Plasmid cp26
Bacteria; Sp
                                                        Borrelia burgdorferi
                                                                                                                                                                  Q9RQR8;
                                                                                                                                                                                 Q9RQR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang I.-N., Dykhuizen D.E., Dunn J., Submitted (OCT-1997) to the EMBL/Ger EMBL, AF029871; AAB8654.1; IR001800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TYEMBLrel. 05, Created)
01-JAN-1998 (TYEMBLrel. 05, Last sequence up
01-JUN-2001 (TYEMBLrel. 17, Last annotation
00TER SURFACE PROTEIN C (FRAGMENT).
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Bacteria: Spirochaetales; Spirochaetaceae; Borr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom;
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194 AA;
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100.08;
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100.08;
                     Spirochaetaceae; Borrelia
                                                        disease
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EMBL/GenBank/DDBJ
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Pred. No.
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                                                        spirochete).
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ID Q44
AC Q44
DT 011
DT 011
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DT 010
DS B0
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CN N
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IQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLE
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Query Match
Best Local Sin
Matches 178;
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Best Local Similarity 100.0%;
Matches 180; Conservative
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"Population dynamics of a naturally oc
Borrelia burgdorferi clones ";
Infect. Immun. 67:5709-5716(1999).
EMBL; AR074465; AAD23912.1;
InterPro; IPR001800; Libopprotein_6.
Pfam; PF01441; Liboprotein_6; 1.
                                                                                                                                                                                                                                                                                     01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-JUN-2001 (TIEMBLIEL 17, Last sequence update)
01-UN-2001 (TIEMBLIEL 17, Last sequence update)
00TER SURFACE PROTEIN C (FRAGMENT)
BOTTELIA BUTGOTÍFII (Lyme disease spirochete)
Bacteria; Spirochaetales; Spirochaetaceae; Borrel
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Q44726;
Q1-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                       Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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Plasmid.
NON_TER 201 201
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SEQUENCE FROM N.A.
STRAIN=3B6';
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                                              NSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGKK 258
IQQNGGLAYEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLE 318
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                                                                                                                                    Similarity
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201 AA;
                                                                                                                      Conservative
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Glass G.E., Childs
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21457
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                                                                                                                                    46.6%;
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%; Pred. No. 3.5
0; Mismatches
                                                                                                                    0;
                                                                                                                    Score 863; DB 2;
Pred. No. 1.3e-33;
0; Mismatches 1
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occurring heterogeneous mixture
                                                                                                                                                                                                                                                                                                                                                                               Steere A.C.;
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3.5e-34;
0;
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Best Local S
Matches 174
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J. Bacteriol. 177:3036-3044(1995).
EMBL; X84783; CAS59254.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_5; 1.
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01-NOV-1996 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
OUTER SURFACE PROTEIN C
                                                                                                                                                                NCBI_TaxID=139;
                                                                                                                                                                                                                                                                    01-MAY-2000 (TIEMBLIEL. 13, Created)
01-MAY-2000 (TIEMBLIEL. 13, Last sequence update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation updat
01-JUR SURFACE PROTEIN C (FRAGMENT).
MEDLINE-94075528; PubMed-8253951;
Theisen M., Frederiksen B., Lebech A.M., Vuust J.,
"Polymorphism in ospC gene of Borrelia burgdorferi
immunoreactivity of OspC protein: implications for
use of OspC protein as a diagnostic antigen.";
J. Clin. Microbiol. 31:2570-2576(1993).
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ProDom; PD001149; Lipoprotein_6; 1.
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Spirochaetaceae; Borrelia
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InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
NON_TER 178 178
SEQUENCE 178 AA; 18894 MW; D619AE
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01-JAN-1998
01-JUN-2001
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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                                          EGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANS
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                                                                                    KIQQNGGLAVEAGHNGTLLAGAYTISKLITQELDGLKNSEKLKEKIENAKKCSEDFTKKL
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Pred. No. 1e-3
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annotation
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Best Local Similarity 97.6
Matches 166; Conservative
  NON_TER
SEQUENCE
                                "Evolution of the Borrelia burgdorferi
J. Bacteriol. 177:3036-3044(1995).
EMBL; X84779; CAA59250.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                       STRAIN-MUL;
MEDLINE-95286481;
                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created 01-NOV-1996 (TrEMBLrel. 01, Last second-JUN-2001 (TrEMBLrel. 17, Last and OUTER SURFACE PROTEIN C (FRACMENT).
                          NON_TER
                                                                                                                                                                                               Borrelia burgdorferi (Lyme disease spirochete).
Bacteria: Spirochaetales; Spirochaetaceae; Borr
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NON_TER 175 175
SEQUENCE 175 AA; 18573 MW. FORE
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Marti-Ras N., Postic D., Foretz M., Baranton G.;

Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; 091792; AAB81889.1; ...

InterPro; IPR001800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6.
                                                                                                                 Hansen K.;
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                                                                                                                                                              SEQUENCE FROM N.A.
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MEDLINE-97478003; PubMed-9336916;

Ras N.M., Postic D., Foretz M., Baranton G.;

"Borrelia burgdorferi sensu stricto, a bacterial species 'made in U.S.A.'?";
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (PRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
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18911 MW;
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                                                        LAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQL 324
                                                                                                                                      tch 44.6%; al Similarity 98.8%; 171; Conservative
                                                                                                                                   Score 826; DB 2; Le
Pred. No. 6.5e-32;
Nismatches 2;
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Search completed: March 18, 2002, 10:10:54 Job time: 977 sec THIS PAGE BLANK (USPTO)

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Perfect score:
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ALIGNMENTS

RESULT AAB62715

03-APR-2001 (first entry)

AAB62715;

AAB62715 standard; Protein; 370

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Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                     WPI; 2001-050113/06.
N-PSDB; AAF29019.
                                                                                                                                         19-JUN-2000; 2000WO-US16915
                                                                                                                                                                                                   Chimeric - Borrelia sp. Chimeric - Borrelia sp.
                                                                                                                                                                                                                                 Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick
                                                                                                                                                                                                                                                    Borrelia sp chimeric ospC protein SEQ
to Lyme disease -
                                                                                                                      18-JUN-1999;
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                                                                    Dattwyler RJ,
                                                                                       (UYNY ) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
                                                                    Seinost G,
                                                                                                                     99US-0140042
                                                                    Dykhuizen D,
                                                                                                                                                                                                                                                       ID NO:
                                                                      Luft BJ,
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                                                                      Gomes-Solecki M;
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                                                 (UYNY ) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC.
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             19-JUN-2000;
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Chimeric -
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                                             WO200078966-A1
                                                                                                Borrelia sp chimeric ospC
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                                                            Borrelia
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              2000WO-US16915.
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                                                                                Lyme disease; vaccine; chimeric protein;
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Best Local Similarity
Matches 323; Conserv
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DB; AAF29020.
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Borrelia
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87.5%; Pred. No. 2.2e-89;
Live 20; Mismatches 25;
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                                                                                                                                    csedftkklegehaqlgienvtdenakkailitdaakdkgaaeleklfkavenlakaake
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                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                   393 AA;
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                        (first entry)
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Pred. No. 3.7e-89;
1; Mismatches 25; 1
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                            359
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Chimeric - Borrelia
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        standard;
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Pred. No. 9.5e
10; Mismatches
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Lyme disease are used
to Lyme disease -
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Chimeric -
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                                                                                                                                                                                        Lyme
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KAAKEMLTNSVKELTS
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DB; AAF29014.
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327; Conser
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Borrelia
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i to immunize
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Pred. No. 1.8e-87;
9; Mismatches 32;
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N-PSDB; AAF29032.
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                                                                                                                                                          Lyme disease.
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                                                                                      KELTSPVVHG-----NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVET
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Borrelia
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                                                                                                                                                                                                     Score 1526; DB 22;
Pred. No. 2.9e-87;
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Best Local Similarity
Matches 326; Conserv
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N-PSDB;
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Lyme disease are used
to Lyme disease -
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(BROO-) BROOK
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DB; AAF29042.
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Pred. No. 3.7
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           121 KLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSV 180
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DB; AAF29022.
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                                                                                                                                                                                                                                                                                                                                                   368 AA;
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Borrelia
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Pred. No. 5.3e-85;
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Best Local Similarity
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                                                                The present invention provides compositions comprising ospC protein chimeric ospC proteins from members of the Borrelia genus. These n Borrelia burgdorferi, B. afzelii or B. garinii. These can be used vaccines against Borrelia infection, which is spread by ticks and
                                              Sequence
                                                              vaccines against Borrelia infection, to Lyme disease.
                                                                                                                                   Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                                                                                              Claim 43; Page 114-115;
                                                                                                                                  to Lyme
                                                                                                                                                                    N-PSDB;
                                                                                                                                                                           WPI; 2001-050113/06
                                                                                                                                                                                             Dattwyler RJ,
                                                                                                                                                                                                                                                                                       WO200078966-A1
                                                                                                                                                                                                                                                                                                        Chimeric -
Chimeric -
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                                                                                                                                                                                                                                      18-JUN-1999;
                                                                                                                                                                                                                                                     19-JUN-2000; 2000WO-US16915
                                                                                                                                                                                                                                                                       28-DEC-2000
                                                                                                                                                                                                                                                                                                                                Borrelia; ospC; Lyme disease;
                                                                                                                                                                                                                                                                                                                                                                  03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                   AAB62725;
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                                                                                                              160pp; English.
                                                                                                                                                                                           Dykhuizen
Score 1488.5; DB 2;
Pred. No. 5.8e-85;
1; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                             vaccine; chimeric protein; tick.
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                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                               ID NO: 54
                                                                                                                                                                                          Luft
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ВJ,
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                 Length
                                                                                                                                                                                        Gomes-Solecki
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to Lyme d
                                                                                   The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelil or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea
                                                                                                                                                                                                                                                                                                                    Compositions of OspC polypeptides 
Lyme disease are used to immunize 
to Lyme disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Chimeric -
                                                                                                                                                                                                                                             Claim 43;
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Length

369;

The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelli or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads

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N-PSDB; AAF29038.
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                                  Claim 43; Page 139-140;
                                                                                                Dattwyler RJ,
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(BROO-) BROOK
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     Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease -
                                       N-PSDB;
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DB; AAF29036.
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Pred. No. 8.7e-85;
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                                                          Gomes-Solecki M;
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Borrelia
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84.1%; Pred. No. 1.16
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                                                                                              Borrelia;
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83.0%; Pred. No. 2e-84;
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                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides compositions comprising ospc proteins and chimeric ospc proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzeli or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions of OspC polypeptides Lyme disease are used to immunize to Lyme disease -
                                                                                                                                                                                                                                                                                                                                                                             vaccines against Borrelia infection, to Lyme disease.
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                                       LKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFES
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DB; AAF29017.
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Post-processing: Minimum Match 0%
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Perfect score:
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1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*

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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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US-08-320-161-1
US-08-320-161-1
US-08-320-161-1
US-08-323-300-161-1
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38.8%; Score 702; DB 4; Length 466; 47.5%; Pred. No. 2.2e-43; tive 54; Mismatches 119; Indels

Indels 18;

Gaps

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Query Match
Best Local Similarity
Matches 173; Conserv

Conservative

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                                                        TELEFAX: (516) 282-372
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acid
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                                                                                                                                NAME: BOGOSIAN, MATGATET C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BLL93-28A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 01-11-93
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CURRENT APPLICATION DATA:

U$\frac{1}{2}\text{08}/235,836C
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                              TOPOLOGY:
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                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-235-836C-110
                                      TELEFAX: (516) 282-37: INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 110,
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                      SEQUENCE CHARACTERISTICS:
                                                                        REGISTRATION NUMBER: 25 324
REFERENCE/DOCKET NUMBER: BNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
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Best Local Similarity 46.3%;
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APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION UNIVERSALE
APPLICATION UNIVERSALE
APPLICATION UNIVERSALE
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MEDIUM TYPE: Floppy
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APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
    LENGTH:
                                                                                                                                 NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324
                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 29-API
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ZIP: 11973
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: NY
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466 amino acids
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                                                                                                                                                                                                                                                                     UMBER: US/08/235,836C
29-APR-1994
                                                        282-3729
                                                                                                                                                                                                                                                                                                                       Release #1.0, Version #1.25
                                      110:
                                                                                                               BNL93-28A
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Pred. No. 3.4e-43;
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TOPOLOGY: 1: ; MOLECULE TYPE: US-08-235-836C-110

protein

Query Match Best Local Similarity

38.3%;

Score 692; DB 4; Pred. No. 1.1e-42;

Length 466

```
TITLE OF INVENTION: ACTIVE proteins from Borrelia TITLE OF INVENTION: burgdorfer1

FILE REFERENCE: 738.001US2

CURRENT APPLICATION NUMBER: US/09/196,293

CURRENT FILING DATE: 1998-11-19

EARLIER FILING DATE: 1998-03-10

EARLIER FILING DATE: 1994-03-10

EARLIER APPLICATION NUMBER: US 07/862,535

EARLIER APPLICATION NUMBER: WO PCT/EP90/02282

EARLIER FILING DATE: 1990-12-21

EARLIER FILING DATE: 1999-12-22

EARLIER FILING DATE: 1999-12-22

EARLIER APPLICATION NUMBER: DE P39 42 728.5

EARLIER APPLICATION NUMBER: DE P40 18 988.0

EARLIER FILING DATE: 1990-06-13

NUMBER OF SEQ ID NOS: 16

SOFTMARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 15

LENGTH: 209
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US-09-196-293-15
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                                                                  ; ORGANISM: Borrelia
US-09-196-293-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Appr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Motz, Manfred
APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fuchs,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKTTLVVKEGTVTLSKNISKSGE 389
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                                                                                   burgdorferi
36.4%;
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Query Match

Score 658.5;

B 4.

Length 209;

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US-08-158-353-3
; Sequence 3, Application US/08158353
; Patent No. 5620862
; GENERAL INFORMATION:
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                                                                                                                                                                                     ; MOLECULE TYPE: US-08-158-353-3
                                                                                                                Matches
                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 145; Conserv
                                                                                                                                                                                                                                                                                        TELEFAX: 617-861-9540 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Carroll, Alice O.
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                     TYPE: amino acid
STRANDEDNESS: sir
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                            60 IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS 119
                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Hamilton, Brook, STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                145;
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Disease
                                                                                                           36.4%; Score 658.5; DB 1; 76.7%; Pred. No. 1.1e-40; Mismatches 30;
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1; Mismatches 30;
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                                                                                                                                         Length 210;
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195 VKELTSPVV 203

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                                                                                                                                                                                                                                                                                Query Match
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Patent No. 67
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MATGARET C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: SNL93-28A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
TRILEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (516) 282-3729
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                            180 VKELTSPVV 188
                                               136 NKLKEKHTDLGKEGVTDADAKEAILKTNGT-KTKGAEELGKLFESVEVLSKAAKEMLANS 194
                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                          77
                                                                                                                                                                          60 IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEEFS 119
                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 VKELTSPVV 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 TKLKDNHAQLGIQGYTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANS 179
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Upton STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                   TKLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANS. 179
                                                                                                             IGKKIHQNNGLDTEYNHNGSLLAGRYAISTLIKOKLDGLK-NEGLKEKIDAAKKCSETFT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKELTSPVV 203
                                                                                                                                                                                                                                                                                                                                                                          l: 210 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0, Application US/08235836C
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                                                                                                                                                                                                                                                            36.18; 76.28;
                                                                                                                                                                                                                                          ; Score 653.5; DB 4;
; Pred. No. 2.5e-40;
11; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.25
                                                                                                                                                                                                                                                                        DB 4; Length 210;
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; Sequence 15, Application US/08209603E
; Patent No. 6248538
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RESULT 8
US-08-209-603E-15
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US-08-235-836C-36
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (516) 282-3729 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION UDATA:
APPLICATION NUMBER: US 08/146
FILING DATE: 01-11-93
FILING DATE: 11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/08235836C Patent No. 6248562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 11973
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,836
FILING DATE: 29-APR-1994
                                                                         193 KELTNPVV 200
                                                                                                          181 KELTSPVV 188
                                                                                                                                      134 KLKDSHAELGIQSVQDDNAKKAILKTHGT-KDKGAKELEELFKSLESLSKAAQAALTNSV
                                                                                                                                                         121 KLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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CITY: Upton
CMATE: NY
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                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                            GKKIKNDGSLDNEANRNESLLAGAYTISTLITOKLSKLNGSEGLKEKIAAAKKCSEEFST 120
                                                                                                                                                                                                                                                                                 ISCNNSG--GDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAI 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282-7338
                                                                                                                                                                                                                                                                                                                                                                       36.0%; Score 652; DB 4; 74.5%; Pred. No. 3.1e-40;
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REFERENCE/DOCKET NUMBER: LKR-
TELECHMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEPAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                  Matches
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: N/A
ANTI-SENSE: N/A
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MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                 ANTI-SENT TYPE: N/A
FRAGINAL SOURCE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/862,535 FILING DATE: 19-JUN-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 10-MAR-1
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS TITLE OF INVENTION: FROM BORRELIA BURGDORFERI NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: DSM 5662
                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                    POSITION IN GENOME:
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US/08/209,603E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
136 NKLKEKHTDLGKEGVTDADAKEAILKTNGT-KTKGAEELGKLFESVEVLSKAAKEMLANS
              120 TKLKDNHAQLGIQGYTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANS 179
                                                                                                                   NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/I
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SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: NEW YORK
STATE: NY
                                                            77
                                                                        60 IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS 119
                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID TOPOLOGY: LINEAR
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                                                        Similarity
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99 PARK AVENUE
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PREAC-MURSIC, VI
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN
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                                                                                                                                                                               36.0%; Score 651.5; DB 4; 76.2%; Pred. No. 3.4e-40; tive 11; Mismatches 31;
                                                                                                                                                                                                                                                                                                                    N/A
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N/A
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                                                                                                                                                                                                            DB 4;
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                                                                                                                                                                                                                                              Query Match 33.0%; Score 597.5; DB 1; Best Local Similarity 69.1%; Pred. No. 2.8e-36; Concerns the 20; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Padula, TITLE OF INVENTION: TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
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195 VKELTSPVV 203
195
              178 NSVKELTSPVVHGN 191
                                                          136 DKLKSSHAELGIANGAATDANAKAAILKTNGT-KDKGAQELEKLFESVKNLSKAAQETLN 194
                                                                            120 TKLKDNHAQLGIQ--GYTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLA 177
                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
                                                                                                                        77
                                                                                                                                        60 IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS 119
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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NSVKELTSPVVAEN
                                                                                                                      IGNLIAQNG-LNAGANQNGSLLAGAYVISTLIAEKLDGLKNSEELKEKIEDAKKCNKAFT 135
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                                                                                                                                                                                                                                                                                                                                                                                                   212 amino acids
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                                                                                                                                                                                                                                                                                                                                                       SS: single
linear
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Methods for Diagnosing Early Lyme
Disease
208
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                                                                                                                                                                                                                                                                           Length 212;
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US-08-031-295-2 ; Sequence 2, Application US/08031295 ; Patent No. 5530103

RESULT 10

GENERAL INFORMATION:

APPLICANT:

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RESULT 11
US-07-903-580-2
; Sequence 2, Application US/07903580
; Patent No. 6221363
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GENERAL,
                                                                                                                                                                                                                                                                                                                                                                                        est Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NIMBER: US 07/824,161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 11-JUL-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/903,580
FILING DATE: 25-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
                                                                                                                                             369
                                                                                                                                                                             140
                                                                                                               200
                                                                                                                                                                                                            309
                                                                                                                                                                                                                                                                                                                       191 NNSGKDGNT-SANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLTSIDELA-KAIG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FITLE OF INVENTION:
                                                                                                                                                                                                                                                                        249
                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                   20 NNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATKAIG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 199303 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: JULY . . . CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                             LTS
                                                                                                                                                                                                    LKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKE 368
                                                                                                                                           LTS 371
                                                                                                                                                                                                                                                                     KKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEFTAK 308
                                                                                                                                                                         LAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANSVKE 199
                                                                                                                                                                                                                                       KKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDFTKK 139
   INFORMATION:
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NVENTION: METHOD AND COMPOSITION FOR THE
NPERTON: PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US 07/727,245
11-JUL-1991
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                                                                                                                                                                                                                                                                                                                                                                  Score 588; DB 1; 1
Pred. No. 1.3e-35;
3; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                 Length 212;
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; Sequence 4, Application (
; Patent No. 5620862
; GENERAL INFORMATION:
; APPLICANT: Padula, St
; TITLE OF INVENTION: N
; TITLE OF INVENTION: I
                                                                                                 RESULT 12
US-08-158-353-4
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Best Local Similarity
Matches 126; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
REFERENCE/DOCKET NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: li
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19920625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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TITLE OF INVENTION: METHOD AND COMPOSITION FOR
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                140
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                                                                                                                                                                 200
                                                                                                                                                                                                369 LTS 371
                                                                                                                                                                                                                                                   309 LKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKE
                                                                                                                                                                                                                                                                                                                                  249
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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STATE: Virginia
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                                                                                                                                                                LTS 202
                                                                                                                                                                                                                                                                                              KKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDFTKK 139
                                                                                                                                                                                                                                                                                                                                                               NNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATKAIG 79
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                 Steven J. Methods for Diagnosing Early Lyme
                                                                                 US/08158353
   Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                               32.5%; Score 588; DB 4; 68.9%; Pred. No. 1.3e-35;
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NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

ADDRESSEE:

E: Hamilton, Brook Two Militia Drive

Brook, Smith & Reynolds, P.C

STREET: I'WO TITY: Lexington

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US-08-35-836C-32
US-08-35-836C-32
Sequence 32, Application US/08235836C
Patent No. 6248562
GENERAL INFORMATION:
APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brookhaven National Laboratory
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: CAITO11, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UC:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 KKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEFTAK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 LKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKE 368
                                                                                                                                                                                                                                                                                                                                                                                                                           200 LTS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 LTS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK 139
                                                         CITY: Upton
STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                   COUNTRY: USA
ZIP: 11973
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TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.001052
CURRENT APPLICATION NUMBER: U$/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: U$ 08/209,603
EARLIER APPLICATION NUMBER: U$ 07/862,535
EARLIER FILING DATE: 1994-03-10
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1992-08-19
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-22
EARLIER FILING DATE: 1990-12-22
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER APPLICATION NUMBER: DE P39 42 728.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09196293 Patent No. 6183755 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fuchs, Renate
APPLICANT: Motz, Manfred
APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
APPLICATE 01-11-93
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: BN TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y Match 30.6%;
Local Similarity 64.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324 REFERENCE/DOCKET NUMBER: BN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 29-APP
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELA-KA 59
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APPLICATION NUMBER: DE P40 18 988.0
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CIP: 10010
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
'CONTOCRETO NUMBER: US/08/209,603E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-209-603E-11
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                                         APPLICATION UMBER: US 07/862,535
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9217-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEPHONE: (212) 697-335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
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US-09-196-293-11
            TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08209603E
Patent No. 6248538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 11
LENGTH: 212
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 30.6%; Score 554; DB 4; Length 212; Best Local Similarity 67.8%; Pred. No. 3.9e-33; Matches 124; Conservative 17; Mismatches 40; Indels
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08
FILING DATE: 10 MAR-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MOTZ, MANFRED
APPLICANT: SOUTSCHECK, ERWIN
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS
TITLE OF INVENTION: FROM BORRELIA BURGDORFERI
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FUCHS, R
APPLICANT: WILSKE,
                                                                                                                                                                   IOR APPLIANCE POT/EFFY, LEATION NUMBER: PCT/EFFY, LEATING DATE: 21-DEC-1990
PTLING DATE: US 07/862,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 LTS 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 LKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKE 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 KKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEFTAK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 NNSGKVGILTSTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKKAIG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OKIDNNNGLAALNNONGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEETNK 139
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WILSKE, BETTINA
PREAC-MURSIC, VERA
                                                                                                                                                                                                                         PCT/EP90/02282
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Search completed: March 18, 2002, 09:55:34 Job time: 347 sec

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CORIGINAL SOURCE:
US-08-209-603E-11
                                                                                                                                                                           Query Match 30.6%; Score 554; DB 4; Length 212; Best Local Similarity 67.8%; Pred. No. 3.9e-33; Matches 124; Conservative 17; Mismatches 40; Indels
                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
IDENTIFICATION INFORMATION:
PUBLICATION INFORMATION:
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
IMMEDIATE SOURCE:
LIBRARY: DSM 5662
                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PROTEIN
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: N/A
                                   200 LTS 202
                      369 LTS 371
                                                309 LKGEHTDLGKEGYTDDNAKKAILKTNNDKTKGADELEKLFESYKNLSKAAKEMLTNSVKE 368
                                                                               POSITION IN GENOME:
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Gaps

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MACNNSGKDGNTSANSADES.....KNLSKAAKEMLTNSVKELTS 371
       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
/cgn2_6/ptodata/2/paa/US60_COMB.pep:
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165.825 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

987654321	Result No.
1809 1804 1801 1801 1564.5 1559.5 1556.5 1556.5	Score
100.0 99.7 99.6 99.6 86.5 86.2 86.0 84.8	
371 370 394 395 370 369 393 375	Length
19 19 19 19 19	DB
US-09-596-746A-34 US-09-596-746-64 US-09-596-746A-64 US-09-596-746A-36 US-09-596-746A-36 US-09-596-746-36 US-09-596-746A-66 US-09-596-746A-66 US-09-596-746A-66	ID
Sequence 34, Appl Sequence 34, Appl Sequence 64, Appl Sequence 64, Appl Sequence 36, Appl Sequence 36, Appl Sequence 66, Appl Sequence 66, Appl Sequence 24, Appl	Description

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-09-596-74	-59	-09-596-74	-596-746-5	-596-746	-596-746A-	-596-746-7	-596-746-4	-09-596-746A	-09-596-74	-09-596-7	-09-596-7	-09-596-7	-09-596-7	-09-596-7	-596-7	-596-7	-09-596-7	-09-596-	-09-596-7	-09-596-7	-09-596-746A-	-09-596-746-7	-09-596-746-3	-09-596-7	-09-596-	-09-596-7	-09-596-746A-	-09-596-74	96-746A-	9-596-746-8	-09-596-746A-	-596-746-6	-09-596-746-2	-09-596-746
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Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	App1	Appl	Appl	Appl	, App1	Appl	Appl	, Appl	Appl	Appl	, Appl	Appl	, Appi	, Appl	, Appl	, Appl	, Appl	, Appl	, Appl	, Appl	Appl	Appl	Appl	Appl	, Appl	, Appl

ALIGNMENTS

Query Match 100.0%; Score 1809; DB 19; Length 371; Best Local Similarity 100.0%; Pred. No. 1.9e-120; Matches 371; Conservative 0; Mismatches 0; Indels 0;	RESULT 1 US-09-596-746A-34 Sequence 34, Application US/09596746A APPLICANT: Dykhutzen, Danial APPLICANT: Dykhutzen, Danial APPLICANT: Luft, Benjamin J. APPLICANT: Luft, Benjamin J. APPLICANT: Luft, Benjamin J. APPLICANT: Luft, Benjamin J. APPLICANT: Luft, Gomes-Solecki TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans FILE REFERENCE: 2631.1002-001 CURRENT FILING DATE: 2000-06-19 PRIOR APPLICATION NUMBER: US/09/596,746A CURRENT FILING DATE: 1999-06-18 NUMBER OF SEQ ID NOS: 84 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 34 LENGTH: 371 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: OspC Chimera US-09-596-746A-34
gth 371; ls 0;	sease in
Gaps	Humans

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Page

TYPE: PAYOU ORGANISM: Artificial Sequence FERTURE: FERTURE: FERTURE: US-09-596-746-34 Ouery Match Best Local Similarity 99.7%; Score 1804; DB 19; Length 370; ON CONSETVATION: OSPC Chimera Ouery Match Best Local Similarity 99.7%; Score 1804; DB 19; Length 370; OY 2 ACMNSGKDGMTSANSADESVKGPMLTEISKKITDSNAVLLAVKEVEALLSSIDELAKAIG OY 2 ACMNSGKDGMTSANSADESVKGPMLTEISKKITDSNAVLLAVKEVEALLSSIDELAKAIG OY 62 KKIKNDGSLDMEANRHESLLAGAYTISTLITOKLSKLNGSEGLKEKIAAAKKSIDELAKAIG OY 122 LKDNHAOLGIGGYDENAKKAILKANAAGKDKGVESLAGAKTIAHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH	PLIT 9-59 9-59 PLIC PLIC PLIC PLIC PLIC PLIC PLIC PLIC	DY 121 KLKDNIHOGIGGVTDENAKKAILITOKLISKINGSEGLKEKIAAAKKCSEEFST 120 DD 121 KLKDNIHOGIGGVTDENAKKAILKANAAGKDKUSKUNGSEGLKEKIAAAKKCSEEFST 120 OY 181 KLKDNIHOLGIGGVTDENAKKAILKANAAGKDKGVEELEKLISGLKEKIAAAKKCSEEFST 120 OY 181 KELTSEPVYHGNNSGKOGNTSANSADESVKGPNILTEISKKLGSELESKIAAKKCSEEFST 120 DD 181 KELTSEPVYHGNNSGKOGNTSANSADESVKGPNILTEISKKLGSELESLIHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	, 4 B
Query Match Matches 369; Conservative 99.7%; Pred. Mo. 7.6e-120; Qy 2 ACNNSGKDGMYSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELAKAIG 61 Qy 2 KKIKNDGSLDNEANRNESULAGAYTISTLITOKLSKLINGSEGLKEKIAAAKKCSEEFSTK 12 Qy 12 LKDNHAQLGIGGVTDENAKAILKANAAGAYTISTLITOKLSKLINGSEGLKEKIAAAKKCSEEFSTK 14 Db 145 LKDHAQLGIGGVTDENAKAILKANAAGKOKGVEELEKLSGSLESLKSKAAKEMLANSVK 121 Qy 12 LKDHAQLGIGGVTDENAKKAILKANAAGKOKGVEELEKLSGSLESLKSKAAKEMLANSVK 121 Qy 182 ELTSPVHGNNSGKDGNTSANSADESVKGPNLTEISKKITGSNAVLLIVIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Sequence 54, Application US/09596746 APPLICANT: Dattwyler, Raymond J. APPLICANT: Seinost, Gerald APPLICANT: Whinizen, Danial TITLE OF INVENTION: Groups of Borrelia burgdorferi and FURENTE OF INVENTION: Borrelia affectif That Cause Lyme Disease in Humans FILE REPERACE, 1263, 1002-00, 16-64 PRIOR APPLICATION NUMBER: US/09/596,746 PRIOR APPLICATION NUMBER: US/09/596,746 SOFTWARE: SEO ID MOS. SOFTWARE: 1999-06-18 SOFTWARE: SEO ID MOS. SEO ID MOS. SEO ID MOS. SEO ID MOS. ORGANISM: OSPC Chimera	Db Oy Db Oy Db Oy Sharing Oy Sharing OS-99-50	us-09-596-746a-34.rapm

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Sequence 36, Application US/09596746A

GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Denttwyler, Raymond J.
APPLICANT: Dykhuizen, Danial
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
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SEQ ID NO 64
FNGTH: 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: 100/9/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
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                                                                                                                                                                                                                                                                                                                     2 LTNSVKELTS 371
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6 LTNSVKELTS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFSTK 121
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7.6e-120;
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                                                                            Cause Lyme Disease in
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; OTHER INFORMATION: OSPC Chimera US-09-596-746-36
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NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 36
LENGTH: 370
                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 36
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                          sequence 36, Application US/09596746 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                               TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                             APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
                                   LENGTH: 369
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                               FEATURE:
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Query Match

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; ORGANISM: OSPC
US-09-596-746-66
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US-09-596-746-66
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SEQ ID NO 66
LENGTH: 393
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Best Local (
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Matches
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
RIOR FILING DATE: 1999-06-18
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                                                     KKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFSTK
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ilarity 87.3%;
Conservative ;
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                                                                                                                                          Score 1556:5; DB 19; Lengt Pred. No. 2e-102; 21; Mismatches 25; Indels
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MLANSVKEL
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; TYPE: PRT; ORGANISM: OSPC Chimera US-09-596-746A-66
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; SOFTWARE: FastSEQ
; SEQ ID NO 66
; LENGTH: 394
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Best Local Sim:
Matches 322;
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APPLICANT:
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/99/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR PILING DATE: 1999-06-18
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361 MLTNSVKEL 369
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                                                                                                      ELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKK
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Pred. No. 2e-102;
1; Mismatches 25;
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US-09-596-746-28
; Sequence 28, Application US/09596746
; GENERAL INFORMATION:
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US-09-596-746A-24
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GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 84.8%; Score 1534;
Best Local Similarity 87.0%; Pred. No. 7.
Matches 328; Conservative 9; Mismatche
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EQ ID NO 24
LENGTH: 375
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR PILING DATE: 1999-06-18
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhulzen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D:
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                                                                                                                                                                                                                                                   SKAAKEMLTNSVKELTS 375
                                                                                                                                                                                                                                                                      SKAAKEMLTNSVKELTS 371
                                                                                                                                                                                                                                                                                                                           VKELTSPVVAESPAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVE
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hes 32;
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelli That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 1090-06-18
PRIOR FILING DATE: 1999-06-18
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CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 378
                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/09596746A GENERAL INFORMATION:
                                                                       NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Wi
SEQ ID NO 28
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
         TYPE: PRT
ORGANISM: Artificial
                                                   LENGTH:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 VKELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 VKELTSPVVHG------NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVK 231
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Pred. No. 8.3e-101;
0; Mismatches 31; 1
                                                                                           Version
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4.

OTHER INFORMATION: OspC Chimera

US-09-596-746A-28

Query Match Best Local Similarity Matches 328; Conserv

Conservative

84.8%; Score 1533.5; DB 19; 86.3%; Pred. No. 8.3e-101; tive 10; Mismatches 31; I

Length 378;

11;

Gaps

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> 61 60

120 TKLKDNHAQLGIQGYTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANS

178

IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLK-NEGLKEKIDAAKKCSETFT IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS 119

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180

Д δÃ 밁 Ωy В

> KAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESV EVETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGEL EVETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGEL VKELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVK VKELTSPVVHG------NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVK 231 NKLKEKHTDLGKEGVTDADAKEAIIKANGT-KTKGAEELGKLFESVEVLSKAAKEMLANS

351

291 238

298

KAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESV

밁 Qy

359 352 299 292 239 232

KNLSKAAKEMLTNSVKELTS 378 KNLSKAAKEMLTNSVKELTS 371

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APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
ILE OF INVENTION: Groups of Borrelia burgdorferi and
ILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-66-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 374
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US-09-596-746-24
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                                                                                                                               Query Match
Best Local Similarity
Matches 327; Conserv
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                                                                                                                                                                                                                                                                   FEATURE:
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61 GKKIKNDGSLDNEANRNESLLAGAYTISTLITOKLSKLNGSEGLKEKIAAAKKCSEEFST 120
                                                       Seinost, Gerald
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                                                                                                                                 Conservative
                                                                                                                                                     84.5%;
87.0%;
                                                                                                                                 Score 1529; DB 19;
Pred. No. 1.7e-100;
9; Mismatches 32;
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; SOFTWARE: FastSI; SEQ ID NO 60; LENGTH: 398; TYPE: PRT; ORGANISM: OSPC (US-09-596-746-60)
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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PRIOR FILING DATE: 1999-(
NUMBER OF SEQ ID NOS: 84:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEI
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                         KLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSV 180
                                                                                                                                                                                      GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLK-NEGLKEKIDAAKKCSETFTN 143
                                                                                                                                                                                                          GKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 4.0
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Maria J.C. Gomes-Solecki
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Seinost, Gerald
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                                                                                                                                                                                                                                                                                               84.4%; Score 1526; DB 19;
86.7%; Pred. No. 3.1e-100;
tive 10; Mismatches 32;
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TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-66-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 60
LENGTH: 399
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; TYPE: PRT
; ORGANISM: OSPC Chimera
US-09-596-746A-60
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US-09-596-746A-60
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Matches 326; Conserv
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Maria J.C. Gomes-Solecki
Dattwyler, Raymond J.
Seinost, Gerald
Dykhuizen, Danial
                                                                                                                  Application US/09596746
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Search completed: Job time: 973 sec

March

18,

2002,

10:08:45

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APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 80
LENGTH: 401
TYPE: PRT
GORGANISM: OSPC Chimera
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                   NLSKAAKEMLTNSVKELTS
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86.0%; Pred. No. 4e-100;
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Title:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptcdata/2/paa/PCT_NEW_COMB.pep:*

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6: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/US10_NEW_COMB.pep:*

8: /cgn2_6/ptcdata/2/paa/US10_NEW_COMB.pep:*
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sequence
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35, Appli
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15045, A
5883, Ap
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Gaps I 60 I 76 I 12 I 13 V 18 V 19		7611, Ap 7611, Ap 18555, Ap 5834, Ap 4824, Ap 123386, Al 7, Appli 12713, Ap 12713, Ap
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RESULT 2 US-09-974-992-3

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CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
LENGTH: 207
TYPE: PRT
ORGANISM: Borrelia garinii
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 7
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              Best Local Similarity Matches 123; Conserv
                                                  Query Match
                                                                                                  LENGTH: 212
TYPE: PRT
ORGANISM: Borrelia afzelii
-09-974-992-7
                                                                                                                                                                                                                                                                                                                                                                      rquence 7, Application US/09974992
NERAL INFORMATION:
APPLICANT: Mathiesen, Marianne J.
APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
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TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
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APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
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                          30.7%;
            19;
                   Score 556; DB 6; Length 212; Pred. No. 2.9e-31;
        Mismatches
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LOCATION: 1..1304
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..1304
OTHER INFORMATION: Ceres Seq. ID 1828628
US-09-708-427-15045
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Best Local Similarity
Matches 102; Conserv
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 15045
LENGTH: 1304
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana FEATURE:
301 CSEEFTAKLKGEHTDLGKEGYTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKB
                                                  361 SIKSELEISQEEKTRALDNEKAATSN-----IQNLLDQRTELSIELERCKVEEEKSKK
                                                                                                                     301 KQLAELNHVLHETKSDNAAQKEKIELLEKTIEAQRTDLEEYGRQVCIAKEEASKLENLVE 360
                                                                                                                                                                                          253 DIEAAKMAESCTNSSVEEWKNKVHELEKEV-----EESNRSKSSASESME----SVM
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                                                                                   -SLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKK 300
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FEATURE: misc_feature
LOCATION: 1..1313
OTHER INFORMATION: Xaa is an INFORMATION: Xaa is an INFORMATION: Xaa is an INFORMATION: 1..1313
OTHER INFORMATION: Ceres Serus-
RESULT 6
US-09-815-242-5883
; Sequence 5883, Application US/09815242
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 15044
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Best Local Similarity
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                               -----:SLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKK
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Pred. No. 7.
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7.3e-05;
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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SEQ ID NO 5883
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APPLICANT: Haselbeck,
APPLICANT: Ohlsen, K
APPLICANT: Zyskind,
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Best Local Similarity
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 NTAMTNLKNGIQDQNTIKQGVNFTDADEAKRNAYTNAVTQAEQILN-----KAQGPNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 NTSANSADESVKGPNLTEISKKITDS-----NAVLLAVKEVEALLSSIDELAKAIGKKIK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 NDG-----SLDNEANRNESLLAGAYTISTLITQKLSKLNGS--EGLKEKIAAAKKC 114
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                                 QHAKDEATALINSSNDLNQAQKDALKQQVQNATT
                                                                  TKGADELEKLFESVKNLSKAAKEMLTNSVKELTS 371
                                                                                                                                                                                          ASQSLGSLDNLNNAQKQTVTDQINGAHTVDEANQIKQNAQNLNTAMGNLKQAIADKDATK 622
                                                                                                                                                                                                                                                                      DASQNKKDAYNNAVTTAQGIIDQTTSPTLDPTVINQAAGQVSTTKNALNGNENLEAAKQQ
                                                                                                                                                                                                                                                                                                                                                   GLSHLTNAQKEALKQLVQQSTTVAEAQGNEQKANNVDAAMDKLRQSIADNATTKQNQNYT
                                                                                                                                                                                                                                                                                                                                                                                        SLESLSKAAKEMLANSVKELTSPVVHGNNSGKDGNTSA-----NSADESV--KGPNLT 214
                                                                                                                                                                                                                                                                                                                                                                                                                               AGVNQVSTTASELNTAMSNLQNGINDEAATKAAL-----NGTQNLEKAKQHANTAID 442
                                                                                                                                              AEI-----EKAKK------CSEEFTAKLKGEHTDLG--KEGVTDDNAKKAILKTNNDK 337
                                                                                                                                                                                                                               VETILTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELK 292
                                                                                                                                                                                                                                                                                                         EIS--KKITESNAVV-----
                                                                                                           ATVNFTDADQAKQQAYNTAVTNAENI I SKANGGNATQAEVEQA I KQVNAAKQALNGNANV
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Zyskind, Judith W.
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Yamamoto, Robert T.
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Trawick, John D.
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 5883
LENGTH: 837
TYPE: PRT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPPLICANT: Bussey, Howard TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits TITLE OF INVENTION: Proliferation FILE REFERENCE: ELITRA.028A CURRENT APPLICATION NUMBER: US/10/072,851 CURRENT FILING DATE: 2002-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                     S--EEFSTKLKD-NHAQLGIQ-GVTDENAKKAILKANAAGKDKGVEELEKLS-----G
                                    TKGADELEKLFESVKNLSKAAKEMLTNSVKELTS 371
                                                                                                                                                 ASQSLGSLDNLNNAQKQTVTDQINGAHTVDEANQIKQNAQNLNTAMGNLKQAIADKDATK
                                                                                                                                                                                                                           DASQNKKDAYNNAVTTAQGIIDQTTSPTLDPTVINQAAGQVSTTKNALNGNENLEAAKQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NDG-----SLDNEANRNESLLAGAYTISTLITQKLSKLNGS--EGLKEKIAAAKKC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTAMTNLKNGIQDQNTIKQGVNFTDADEAKRNAYTNAVTQAEQILN-----KAQGPNTS 331
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QHAKDEATALINSSNDLNQAQKDALKQQVQNATT 716
                                                                                                            AEI-----EKAKK------CSEEFTAKLKGEHTDLG--KEGVTDDNAKKAILKTNNDK 337
                                                                                                                                                                                   VETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELK 292
                                                                                                                                                                                                                                                            EIS--KKITESNAVV-----
                                                                            <u>ATVNETDADQAKQQAYNTAVTNAENIISKANGGNATQAEVEQAIKQVNAAKQALNGNANV</u>
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Zyskind, Judith W.
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Boone, Charles
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Zamudio, Carlos
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22.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 187; DB 7;
Pred. No. 4.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183;
                                                                                                                                                                                                                                                               -----LAVKE 232
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SOFTWARE: FastSEQ for
SEQ ID NO 13080
LENGTH: 875
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Best Local
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PRIOR
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
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CURRENT FILING DATE: 2001-03-21
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338 TKGADELEKLFESVKNLSKAAKEMLTNSVKELTS
                                                        660 ATVNFTDADQAKQQAYNTAVTNAENIISKANGGNATQAEVEQAIKQVNAAKQALNGNANV 719
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                                                                                                                                                                                   VETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELK 292
                                                                                                                                                                                                                                                                                                                                                                                                                          S--EEFSTKLKD-NHAQLGIQ-GVTDENAKKAILKANAAGKDKGVEELEKLS------G 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDG-----SLDNEANRNESLLAGAYTISTLITQKLSKLNGS--EGLKEKIAAAKKC 114
                                                                                                  AEI----EKAKK-----CSEEFTAKLKGEHTDLG--KEGVTDDNAKKAILKTNNDK 337
                                                                                                                                             ASQSLGSLDNLNNAQKQTVTDQINGAHTVDEANQIKQNAQNLNTAMGNLKQAIADKDATK
                                                                                                                                                                                                                                 DASQNKKDAYNNAVTTAQGIIDQTTSPTLDPTVINQAAGQVSTTKNALNGNENLEAAKQQ
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Xu, H. Howard
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Pred. No. 4.6e-05;
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US-10-072-851-13080
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13080, Appl GENERAL INFORMATION:
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Best Local Similarity
Matches 101; Conserv
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ATTLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
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                       720 QHAKDEATALINSSNDLNQAQKDALKQQVQNATT 753
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                                                                                                                                                                                        ASQSLGSLDNLNNAQKQTVTDQINGAHTVDEANQIKQNAQNLNTAMGNLKQAIADKDATK
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                                                            TKGADELEKLFESVKNLSKAAKEMLTNSVKELTS 371
                                                                                                      ATVNFTDADQAKQQAYNTAVTNAENI I SKANGGNATQAEVEQA I KQVNAAKQALNGNANV
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                                                                                                                                             AEI-----EKAKK-------CSEEFTAKLKGEHTDLG--KEGVTDDNAKKAILKTNNDK
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Yamamoto, Robert T
Roemer, Terry
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Zyskind, Judith W.
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Zamudio, Carlos
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; Pred. No. 4.6e-05;
62; Mismatches 183
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US-10-032-585-7646
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; GENERAL INFORMATION:
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TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7646
LENGTH: 1881
TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                         Sequence 15590, Application US/10072851 GENERAL INFORMATION:
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Best Local Similarity 22.6
Matches 101; Conservative
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APPLICANT:
APPLICANT:
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  APPLICANT:
                       APPLICANT
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LOCATION: (1881)..(1881)
OTHER INFORMATION: X-any amino acid
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                                    Foulkes, J. Gordon
Zamudio, Carlos
Ohlsen, Kari L.
                                                                                  Xu, H. Howard
                       Haselbeck, Robert
                                                                                                          Grant J.
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Gaps

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RESULT 12
US-09-708-427-19883
; Sequence 19883, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS;
; TITLE OF INVENTION: THEREBY
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; NAME/KEY: MISC_FEATURE
; LOCATION: (1881)..(1881)
; OTHER INFORMATION: X-any amino acid
US-10-072-851-15590
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APPLICANT: Bussey, Howard

TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits

TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits

TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits

TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits

THE EFFERNCE: ELITRA, 028A

CURRENT FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 15811

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 1881

TYPE: PRI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 NAVVLAVKEVETLLTSIDELAKAIGK-----KIKNDVSLDNEADHNGSLISGAYLISNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 ITKKISAIKDSGELKA-----EIEKAK-------KCSEEFTAKLKGEHTDLGK-- 318
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Boone, Charles
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Yamamoto, Robert T.
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                                                AND CORRESPONDING POLYPEPTIDES
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: NAME/KEY: misc_feature

: LOCATION: 1..1014

: OTHER INFORMATION: Ceres Seq. ID 1836847

US-09-708-427-19883:
                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19882
LENGTH: 1018
                                                                                                                                                                                                                                                                                    Sequence 19882, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEO ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1983
LENGTH: 1014
TYPE: PRT
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Best Local Similarity
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NAME/KEY: misc_feature
LOCATION: 1..1018
OTHER INFORMATION: Xaa is any amino
NAME/KEY: misc_feature
LOCATION: 1..1018
                                                                                                      ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                TYPE: PRT
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Pred. No. 0.0003;
31; Mismatches 15
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NAME/KEY: misc_feature
LOCATION: 1..1269
OTHER INFORMATION: Xaa is al
NAME/KEY: misc_feature
LOCATION: 1..1269
OTHER INFORMATION: Ceres See
US-09-708-427-19881
                                                                                                                                                                                                                                                                                                             US-09-708-427-19881
US-09-708-427-19881, Application US/09708427

; Sequence 19881, Application US/09708427

; GENERAL INFORMATION: THEREBY

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243p

; CURRENT APPLICATION NUMBER: US/09/708,427

; CURRENT FILING DATE: 2000-11-09

; NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1

EQ ID NO 19881
LENGTH: 1269

TYPE: PRT

; ORGANISM: Arabidopsis thaliana
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Best Local S
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66 NDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFSTKLKDN 125
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                                                                               SADESY--KGPNLTEISKKITDSNAY--LLAVKEVEALLSSIDEL-----AKAIGKKIK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLKENVENAATASVKVAELTS 870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVL--AVKEVETLLTSIDEL
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                                                SAEESLEQKGREIDEATTKRMELEALHQSLSIDSEHRLQKAMEEFTSRDSEASSLTEKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDQAQEKSLQSSSESELLAETNNQLKIK-IQELEGLIGSGSVEKETALKRLEEAIERFNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
                                                                                                                             h 9.8%;
Similarity 24.4%;
                                                                                                              Conservative
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                                                                                                           Pred. No. 0.0004;
Mismatches 152;
                                                                                                                                            Score 176.5;
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                                                                                                 US-09-708-427-15046
Sequence 15046, Application US/O GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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                                                                                                                                                                                                                                                                                                                                                      1047
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                                                                                                                                                                                                                                                                                        NLSKAAKEMLTNSVK--ELTS
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                                                                 Application US/09708427
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NAME/KEY: misc_feature
COCATION: 1.1144
OTHER INFORMATION: Xaa is:
NAME/KEY: misc_feature
COCATION: 1.1144
OTHER INFORMATION: Ceres S.
US-09-708-427-15046
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                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 29.3 Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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  VSTLKT-IDELSDLKQSLIHKEKELQAAIVENEKLKAEAALSLQRIEELTNLKQTLIDKQ
                                                                                    NKENELHGMVVEIEDL-RSKDSLAQKKIEELSNFNASLLIKE-NELQAVVCENEELKSKQ
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                                                                                                                            NSVKELTSPVVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVV-----LAVKE
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Search completed: March 18, 2002, 09:58:23 Job time: 381 sec

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Title:
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A;Gene:
C;Superf
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A;Molecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-210 <RES>
A;Cross references: EMBL:U04281; NID:9434663; PIDN:AAC43297.1; PID:9434664
A;Cross references: EMBL:U04281; NID:9434663; PIDN:AAC43297.1; PID:9434664
A;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in OspC variation A;Reference number: S70255; MUID:96296448
A;Accession: S70282
                                                                                                                                                                A;Cross-references: EMBL:L42893; NID:g858721; A;Experimental source: strain 297
                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 19-210 <LIV>
                                                                                                                                                                                                                                       A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                              tevenson, B.; Barthold, S.W. Microbiol. Lett. 124, 367-372, 1994
A/Title: Expression and sequence of outer surface A;Reference number: I40143; MUID:95154673
A;Accession: I40144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outer surface protein C precursor - Lyme disease spirochete C; Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_che C;Accession: I40144; S70282
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I40144
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A;Accession: S69918
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-211 <JAU>
A;Cross-references: EMBL:X81522; NID:9872021; PIDN:CAA57242.1; PID:9872022
A;Experimental source: strain PBre
R;Roessler, D.
Submitted to the EMBL Data Library, September 1994
A;Accession: $72674
A;Accession: $72674
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A;Residues: 1-152,'E',154-211 <ROE>
A;Cross-references: EMBL:x81522; NID:g872021; PIDN:CAA57242.1;
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0; Mismatches
                               Score 879;
Pred. No. 5.
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Pred. No. 3.5e-34;
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outer surface protein C - Lyme disease spirochete (strain HUR) (fragment) C; Species: Borrella burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 *sequence_revision 02-Aug-1996 *text_change 26-May-200 C;Accession: I40106; S54185 R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, A.M.; H. J. Bacteriol. 177, 3036-3044, 1995 A;Title: Evolution of the Borrelia burgdorferi outer surface protein Ospc. A;Reference number: I40104; MUID:95286481
A:Status: preliminary; translated A:Molecule type: DNA A:Residues: 1-178 <RES>
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R;Theisen, M.; Frederiksen, B.; Lebech, A.M.; Vuust, J.; Hansen, K.
J. Clin. Microbiol. 31, 2570-2576, 1993
A;Title: Polymorphism in ospC gene of Borrelia burgdorferi and immunoreact A; Reference number: I40105; MUID:94075528
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A; Residues: 1-203 < RES>
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Best Local
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                                                                                                                                                                                                                                                                                                                          KELTSPV 187
                                                                                                                                                                                                                                                                                                                                                       KLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSV
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95.78;
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                              from GB/EMBL/DDBJ
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Pred. No. 3.1e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 203
                                                                                                                  Lebech, A.M.; Hansen,
                                                                                                                                                  26-May-2000
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A;Cross-references: E
C;Genetics:
A;Gene: ospC
C;Superfamily: Lyme c
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A;Variety: strain PKa
C;Date: 15-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-May-2000
C;Accession: S69927; S72669
C;Accession: S69927; S72669
C;Accession: S69927; Liegl, G.; Preac-Mursic, V.; Roessler, D.; Schwab, E.;
J. Clin. Microbiol. 33, 1860-1866, 1995
A;Title: Molecular analysis of genes encoding outer surface protein C (OspC)
A;Reference number: 140047; MUID:95395018
A;Accession: S69927
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A; Residues: 1-124,'D',126-139,'E'
A; Cross-references: EMBL:X69589
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A; Residues: 1-210 < JAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outer surface protein C precursor - Lyme disease spirochete (strain C; Species: Borrelia burgdorferi (Lyme disease spirochete)
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                  uperfamily: Lyme disease spirochete surface
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 195
                                    180
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                                                                                         TKLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELAKAIGKKIKNDGSL
                                                                                                                                                               IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS 119
                                                                                                                                                                                                                   ISCNNSGRDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFSTKLKDNHAQLG
VKELTSPVV 203
                                    VKELTSPVV 188
                                                                      NKLKDKHTDLGKEGVTDADAKEAILKTNGT-KTKGAEELGKLFESVEVLSKAAKEMLANS
                                                                                                                                            IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLK-NEGLKEKIEAAKKCSETFT
                                                                                                                                                                                                                                                                                           146;
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                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                        36.7%;
77.2%;
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Pred. No. le-32;
                                                                                                                                                                                                                                                                                                          Score 663.5; DB 2
Pred. No. 3.8e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 February 1994
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outer surface protein C - Lyme disease spirochete C;Species: Borrella burgdorferi (Lyme disease spirochete) C;Species: Borrella burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000 C;Accession: G70218; I40269; S37726; S70281
C;Accession: G70218; I40269; S37726; S70281
C;Accession: G70218; I40269; S37726; S70281
Spirochete, G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                          Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease
A; Reference number: A70100; MUID:98065943
A; Accession: G70218
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C;Superfamily: Lyme disease spirochete surface
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Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and
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                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-210 <RES>
                                                                                                                                    R;Fukunaga, M.; Hamase, A.
J. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence
A;Reference number: 140269; MUID:96025162
A;Accession: 140269
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A;Experimental source: strain 28354
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A; Residues: 1-193 <LIV>
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A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Med. Microbiol. Immunol. 182, 37-50, 1993
                                                                                                                                                                                                                                                            A;Cross-references: GB:AE000792; NID:g3253098; A;Experimental source: strain B31
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                                                                                                                                                                                                                                                                                                          A;Mòlecule type: DNA
A;Residues: 1-210 <KLE>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKK
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Pred. No. 4.1e-24;
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                                                                                                                                                                                            Borrelia
                          ; PID:g769684
Schwab, E.;
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B 선 동

Genetic heterogenity of the genes coding for the outer surface

protein C Soutschek,

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A;Reference number: S3772b; mulling.
A;Reference number: S3772b; mulling.
A;Accession: S37726
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-210 < JAUD
A;Cross references: EMBL:X69596; NID:g311391; PIDN:CAA49306.1; PID:g311392
A;Title: Evidence for lateral transfer and recombination in OspC variation
**Poference number: S70255; MUID:96296448
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                                                                                                                                                                                                                               A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X73626; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
I40122
                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-200 < RES>
                                                                                                                                                                                                                                                                                                                                                                     R;Theisen, M.; Frederiksen, B.; Lebech, A.M.; Vuust, J.; Ha
J. Clin. Microbiol. 31, 2570-2576; 1993
A;Title: Polymorphism in ospC gene of Borrelia burgdorferi
A;Reference number: I40105; MUID:94075528
                                                                                                                                                                                                                                                                                                                                                                                                                                      outer surface protein C - Lyme disease spirochete (strain DK6) (fragment) Cispecies: Borrelia burgdorferi (Lyme disease spirochete) te: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-20 ccession: I40122; S34177
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A; Residues: 19-210 <LIV>
A; Cross-references: EMBL: L42887; NID: g858715;
                                                                                                                                                    Query Ma
Best Loo
Matches
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Best Local Similarity 76.7
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                 GKKIKNDGTLDNEANRNESLIAGAYEISKLITQKLSVLN-SEELKEKIKEAKDCSEKFTT
                                                                                                 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELAKAI 60
                                                  GKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFST 120
                                                                                  ISCNNSG--GDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAI
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                                                                                                                                                      al Similarity
141; Conserv
                                                                                                                                                      Conservative
                                                                                                                                                                  36.38;
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76.7%; Pred.
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                                                                                                                                                  Score 656; DB
Pred. No. 8e-2
0; Mismatches
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R;Livey, I.; Gibbs, C.P.; Schuster, R.;
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer
A;Experimental source:
C;Genetics:
                                                                                                          A; Molecule type: DNA
A; Residues: 1-193 <LIV>
                                                                                                                                                                                                                        A; Reference number: S70255; MUID:96296448 A; Accession: S70286
                                                                                                                                                                                                                                                                                                                                                                                                         outer surface protein C - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_C;Accession: $70286
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A;Residues: 1-207 </AU>
A;Ressidues: 1-207 </AU>
A;Cross-references: EMBL:X83554; NID:g872027; PIDN:CAA58544.1; PID:g872028
A;Cross-references: EMBL:X83554; NID:g872027; PIDN:CAA58544.1; PID:g872028
A;Experimental source: strain PTrob
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, JaC;Genetics:
                                                                      A;Cross-references: EMBL:L42897; NID:g858728; PIDN:AAB37006.1; PID:g1695222
                                                                                                                                                                                 A; Status: nucleic acid sequence
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A;Title: Molecular analysis of genes encoding outer surface protein C (OspC) of A; Reference number: I40047; MUID:95395018
A; Accession: S69919
A; Status: nucleic acid sequence not shown; translation not shown
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A;Variety: strain PTrob
C;Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: ospC
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1860-1866, 1995
                                                                                                                                                                                                                                                                                                                                                                      Schuster, R.;
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75.0%;
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RESULT 12

S37727

outer surface protein C precursor - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-May-2000
C:Accession: S37727
R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschwad, Microbiol, Immunol. 182, 37-50, 1993
A;Title: Genetic heterogenity of the genes coding for the outer surface protein A; Reference number: S37726; MUID:93268136
A;Accession: S37727
A;Status: preliminary
A;Mclecule type: DNA
A;Residues: 1-207 <JAU>
A;Residues: 1-207 <JAU>
A;Residues: EMBL:X69595; NID:g311393; PIDN:CAA49305.1; PID:g311394
                             RESULT 13
570276
outer surface protein C - Lyme disease spirochete
c:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change
C:Accession: S70276
R:Livey, I: Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
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74.5%; Pred. No. 9.4e-24;
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A; Reference number: S70255; MUID:96296448
A; Accession: S70276
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-193 <LIV>
A; Cross-references: EMBL:L42890; NID:9858718
A; Experimental source: Strain E61
C; Genetics:
A; Cross-references: EMBL:A2890; NID:9858718
                                                                                                                                                                                                                                                                                                                                                                 R:Stevenson, B.; Barthold, S.W.

PEMS Microbiol. Lett. 124, 367-372, 1994
A:Title: Expression and sequence of outer surface A:Reference number: I40143; MUID:95134673
A:Accession: I40143
                                                                                                                                                                                                                                                       A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
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C;Superfamily: Lyme disease spirochete surface
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C;Genetics:
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Outer surface protein C precursor - Borrelia garinii
C:Species: Borrelia garinii
C;Species: Borrelia garinii
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 26-May-2000
C;Accession: I40271
R;Fukunaga, M.; Hamase, A.
J. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence analysis of Borrelia burgdorferi sensu la
A;Reference number: I40269; MUID:96025162
A;Accession: I40271
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 17207 <RES>
A;Cross-references: GB:D49377; NID:g1041103; PIDN:BAA08375.1; PID:g1041104
C;Superfamily: Lyme disease spirochete surface protein C
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GenCore version (c) 1993 - 2000

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2002, 10:11:49; Search time 39.62 Seconds

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Scoring table:

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Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A. Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Han van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
                                                                                                                                                            "Outer surface protein C gene sequence analysis burgdorferi sensu lato isolates from Japan.";
J. Clin. Microbiol. 33:2415-2420(1995).
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STRAIN-ATCC 35210 / B31;
MEDLINE-94041630; PubMed-8225587;
MEDLINE-94041630; PubMed-8225587;
Padula S.J., Sampieri A., Dias F., Szczepanski A., Ryan I Molecular characterization and expression of p23 (OspC) American strain of Borrelia burgdorferi.";
Infect. Immun. 61:5097-5105(1993).
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Plasmid 1p54.
Bacteria; Spirochaetales; Spirochaetaceae; Bor
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Jauris-Heipke S.,
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15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
OUTER SURFACE PROTEIN C PRECURSOR (PC).
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; U01894; AAA16058.1; -.
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1; Mismatches 30;
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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J. Clin. Microbiol. 31:2570-2576(1993).
J. FUNCTION: NOT KNOWN, MAJOR INMUNODOMINANT PROTEIN.
J. SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE
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[2]
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Mol. Microbiol. 6:3299-3311(1992).

-I- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.

-I- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPII
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SEQUENCE
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SEQUENCE FROM N.A.

STRAIN-SSP. HS1 SEROTYPE 3;

MEDLINE-93133110; PubMed-1484486;

Restrepo B.I., Kitten T., Carter (
"Subtelomeric expression regions (
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ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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                                                                                                                                                                  Bacteria;
                                                                                                                                                                                        Plasmid
                                                                                                                                                                                                           Borrelia hermsii.
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MEDLINE-93133110; PubMed-1484486;
                                                                                                                                        NCBI_TaxID=140;
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el. 26, Last sequence update)
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OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR
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Pred. No. 2.4e
32; Mismatches
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    C.J.,
    Borrella
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    Infante D., Ba
rrelia hermsii
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           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                             Schizosaccharomyces pombe (Fission yeast) Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entitles requires a license agreement (See http://www.isb
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MO1. Microbiol. 6:3299-3311(1992).
-i- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
                                                             Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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proDom; pD001149; Lipoprotein_6; 1.
prOSITE; pS00013; pROKAR_LIPOPROTEIN;
                                                                                         STRAIN=972;
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                    SPAC1F3.06C.
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215 AA;
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(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
L 222.8 KDA PROTEIN C1F3.06C IN CHROMOSOME
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                                                                                                                                                                                                                                                                                 STANDARD;
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Pred. No. 1.7e-10;
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N-ACYL DIGLYCERIDE
; 684C74D35F87C771
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                MEDLINE-92315338; PubMed-1617731; MEDLINE-92315338; PubMed-1617731; Galinski M.R., Medina C.C., Ingrama reticulocyte-binding protein comerozoites.";
                                                                                                                                                                                                 Plasmodium vivax (strain Eukaryota; Alveolata; Api NCBI_TaxID=31273;
                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last seq
01-OCT-1996 (Rel. 34, Last ann
RETICULOCYTE BINDING PROTEIN 2
                                                                                                 Cell 69:1213-1226(1992)
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                                                  FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECHUMAN RETICULOCYTE CELLS.
SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE).
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PROTEIN 2 (FRAGMENT).
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Best Local S
Matches 104
                            protein
J. Cell
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                                                                                            STRAIN=X2180-1A; MEDLINE=91185402; PubMed=2010462;
                                                                                                                                                                                                                     01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.
 SEQUENCE OF
                                                                                  Nakajima
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                   Eukaryota; Fungi; i
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                   1061
                                                   "A cytoskeleton-related gene, uso1,
                                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
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                                                                     lamasaki M.;
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                         transport in Saccharomyces Biol. 113:245-260(1991).
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                                                                                                                                                                 Ascomycota; Saccharo; Saccharomycetaceae;
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3; Mismatches
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                                                                                Yonehara
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                                                                                Yoda
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EMBL; L03188; AAB00143.1; -.
EMBL; U53668; AAB66659.1; -.
PIR; A38455; A38455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-8 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [nterPro;
 251
                                                                                                                                        159
                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEMBRANES. PROBABLY PRESENT ON VESICIER AND THE GOLGI COMPLEX.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS
OF AN HEPTAPEPTIDE BEDDAM CAMMINIST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL. SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: MEMBRANES. PROBABLY PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: REQUIRED
                                                                                                                                                                                                                                                                             KEYEALLSSIDELAKAIGKKI-KNDGSLDNEANRNESLLAGAYTISTLITQKLSKLN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; P80220; 1DIP.
S0002216; USO1
                                KKKNDELEGEVKAMKSTSEEQSNLKKSEIDALNLQIKELKKKNETNEASLLESIKSVESE
                                                                                                    NSLRANLESLEKEHEDLAAQLKKYEEQIANKERQYNEEISQLN----DEITSTQQENESI
                                                                                                                                      EKLSGSLESLSK-----AA-----KEMLANSVKELTSPVVHGNNSGKDGNTSANSADESV
                                                                                                                                                                                                                                             KNIEQLKKTISDLEQTKEEIISKSDSSKDEYESQISLLKEKLETATTANDENVNKISELT
IKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSG----ELKAEIEKAKKCSEEFT
                                                                                                                                                                      KTREELEAELAAYKNLKNELETKLETSEKALKEVKENEEHLKEEKIQLEKEATET-KQQL
                                                                                                                                                                                                          -GSEGLKEKIAAAKKCSEEFSTKLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                 ; 68
                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Symington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                   725
465
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924
1253
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1660
1661
1772
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                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      724
1790
487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transport;
                                                                      ---LTEISKKITESNAVVLAVKEV----
                                                                                                                                                                                                                                                                                                                               9.9%;
23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spectrin.
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                                                                                                                                                                                                                                                                                                                                                                                                   206424
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                                                                                                                                                                                                                                                                                                                                                                                     GLOBULA HEAD.

COLLED COIL (POTENTIAL).

COLLED COIL (POTENTIAL).

CHARGED (HYPER-HYDROPHILIC).

DISPENSABLE FOR THE PROTEIN FU

ASP/GLU-RICH (ACIDIC).

G -> E (IN REF. 2).

E -> K (IN REF. 2).

V -> I (IN REF. 2).

I -> V (IN REF. 2).

N -> S (IN REF. 2).

O -> S (IN REF. 2).

R -> S (IN REF. 2).

R -> S (IN REF. 2).

R -> S (IN REF. 2).

C -> D -> DEEDDEE (IN REF. 2).

C -> D -> DEEDDEE (IN REF. 2).
                                                                                                                                                                                                                                                                                                                 68;
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PROTEIN TRANSPORT
                                                                                                                                                                                                                                                                                                             Score 178.5; |
Pred. No. 0.54
68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Golgi stack; Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ON VESICLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSOCIATED WITH INTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           нісніх
                                                                                                                                                                                                                                                                                                                                 . 54 ;
                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                               156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATIONAL BETWEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPETITIVE,
                                                                  ETLLTSIDELAKAIGKK
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coiled
                                                                                                                                                                                                                                                                                                                                                 1790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO THE GOLGI
                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOSED
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                                                                                                                                                                                                                                                                                                             Gaps
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306
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1257

TVKIKELQDECNFKEKEVSE-----LEDKLKASEDKNSKYLELQKESEKIKEELDAKT

Matches 100;

Similarity

Conservative

56;

Mismatches

Indels 128;

Gaps

19;

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M12_STRPY
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  Query Match
Best Local 9
                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                 TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for conmodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1310
                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 169:5633-5640(1987).
-!- FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SERVICE OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CS24 / Serotype M12;
MEDLINE-88058777; PubMed-2445730;
Robbins J.C., Spanier J.G., Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1370 KLLNEGSSTITQEYSE 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P19401;
01-NOV-1990
                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                                                                                                             Virulence; Phagocytosis;
                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001899; Gram_pos_anchor
InterPro; IPR003345; M_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A60115; A60115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M18269; AAA88573.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMM12
                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L2_STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL. SIMILARITY: TO OTHER M PROTEINS. SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: TO OTHER M PROTEINS. SIMILARITY: TO OTHER STREPTOCOCCAL AN IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHAGOCYTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLSKAAKEMLTNSVKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKLK - - - GEHTDLGKEGVTDDNAKKAILKTNNDKTKGADE - LEKL - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                             PF00746; Gram_pos_anchor;
                                                                                                                                                                                                                                                                                                                                                                                                            PF02370; M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEROTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel.
                                                                                                564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169:5633-5640(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spanier J.G., Jones pyogenes type 12 M
                                                                                                  8
                                                                                                                                                                                                                                                                                                                                       Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD.
                                                                                                                                                                     >564
550
>564
505
541
547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16, Last sequence up
                                                                                                564
62904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 PRECURSOR (FRAGMENT).
9.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                           Cell wall;
                                                                                                  ¥.
                                                                                                                                                                                                                                                                                                                                signal.
  Score 173;
Pred. No. 0
                                                                                                                                                             MEMBRANE ANCHOR.
COILED COIL (POTENTIAL).
GLY/PRO-RICH (CELL WALL-SPANNING)
CONSERVED IN GRAM-POSITIVE COCCI
                                                                                                                                                                                                                                                           M PROTEIN, SEROTYPE
EXTRACELLULAR (POTEN
                                                                                                                                              PROTEINS
                                                                                                5F1549DACAA77B46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.J., Simpson W.J., protein gene regula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on update)
                                                                                                                                                                                                                                                                                                                                                             Duplication; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ⋛
                        DB 1;
                                                                                                                                                                                                                                                                ROTYPE 12.
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STAPHYLOCOCCAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulation
                      Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Cleary
ation by
                                                                                                                                                                     COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                             Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -FESVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            တ္က
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MYSN_ACACA
ID MYSN_A
AC P05659
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                                                                                                                                                                                                                                                                                                                                                              Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.;

"Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle myosin heavy chain gene from Acanthamoeba: evidence of a hinge in the rodilke tail.";

J. Cell Biol. 105:913-925(1987).

-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

-I- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALLIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS
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       modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P05659;
01-NOV-1988 (Rel.
01-NOV-1988 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87308395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, 1
20-AUG-2001 (Rel. 40, 1
MYOSIN II HEAVY CHAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                             CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INVERRUPTED BY A HINGE AND JOINED BY A NONHELICAL TAILDIECE WHERE THE REGULATORY PHOSPHORYLATION SITES RESIDE.

THE REGULATORY PHOSPHORYLATION SITES RESIDE IN MEDIATING REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTIVITY. SIMILARITY: CONTAINS 1 MYOSIN LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 2 IQ DOMAINS.
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Bacillus/Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAGSNYVGATIGEKAIDKLK----ASVSKEVTE------QYTKVIFDNFKDIAKGLSD
                       --YLISNLIT----KKISAIKDSGE-LKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDD
                                                                                                                                                                                                                           LESLSKAAKEMLANSVKELTSPVVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESN
                                                                                                                                                                                                                                                                                                                     FSTK---LKDNHAQL--GIQ-----GVTDENAKKAILKAN--AAGKDKGVEELEKLSGS
FDQILSQLPTADQLPDIATIKSSLEDVKAQVAQV-KAMPEATSKLY--
                                                                                     KSETAMKEFKKQLTDFENSLKNRDQAFKNVINSSDFLTAEQKSQLINSVEKKLPQVDAPD
                                                                                                                                AVVLAVKEVETLLTSIDELAKAIGKKIKNDVSLDN--EADHNGSLISGA--
                                                                                                                                                                                LQNVQKGTPN-LTNGLDQLNSKV------QEGSEKAAKAEKIINALDLTKLETAVNNLE
                                                                                                                                                                                                                                                                          ISDKTAQLADGAAQVTSGIQSLDSSLGKFQDSSNQIYDKSSQLAAGSGELTSKMNELLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y14083; CAA74522.1;
M97208; AAA22521.1;
Z99109; CAB12856.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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n; Transmembrane;
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Last sequence update)
Last annotation update)
PROTEIN IN HEMY-GLTT INTERGENIC REGION (ORFB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Clostridium group;
us group; Bacillus.
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ne EMBL/GenBank/DDBJ (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 169.5;
Pred. No. 0.53
74; Mismatches
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POTENTIAL.
POTENTIAL.
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434
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RESULT 11
C -!- FUNCTION: MUSCLE CONTRACTION.

C -!- SUBURIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

HEXAYY CHAIN SUBURITS (MEC), 2 ALKALI LIGHT CHAIN SUBURITS (MLC)

C HEXAYY CHAIN SUBURITS (MEC), 2 ALKALI LIGHT CHAIN SUBURITS (MLC)

C HEXAYY CHAIN SUBURITS (MEC), 2 ALKALI LIGHT CHAIN SUBURITS (MLC-2),

C HEXAYY CHAIN SUBURITS (MIC-2),

C -!- SIBGELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

C -!- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

C -!- SUBCELLULAR RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

C (YCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

C CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

C -!- MISCELLANEOUS: FOR ALPHA-HELICAL COILED COILS.

C -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE

SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS ($1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYSC_CA
P12845;
                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Karn J., Dibb N.J., Miller D.M.; "Cloning nematode myosin genes."; Cell Muscle Motil. 6:185-237(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dibb N.J., Maruyama I.N., Krause M. "Sequence analysis of the complete heavy chain gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989
20-AUG-2001
                                                                           EMBL;
                                                                                                                                                      entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BRISTOL N2;
MEDLINE=85201409; PubMed=3888374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
MEDLINE-89178677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-21; 112-371 AND 1501-1772
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                                                                                            EMBL;
                                                                                                          EMBL;
                                                                                                                                         or send an
                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                -! - MISCELLANEOUS:
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                                        NL; X08066; CAA30855.1; -.
NL; M37233; AAA28121.1; -.
NL; M37235; AAA28122.1; -.
NL; M37236; AAA28123.1; -.
NL; S05697; S05697.
                                                                                                                                                                                                                                                                                                               SUBFRAGMENT (S2)
                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboratien the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAEEL
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                                                                                                                                                    requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370
                                                                                                                                       equires a license agreement (See email to license@isb-sib.ch).
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(Rel.
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(Rel. 12,
(Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=2926820;
ma I.N., Krause M.,
                                                                                                                                                                                                                                                                                                THERE ARE FOUR DIFFERENT MYOSIN HEAVY
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Last annotation update)
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for
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EMBL; PIR;

InterPro;

IPR002928; IPR001609;

Myosin_tail.
myosin_head.

4

HSSP; P08799; 1MND

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Best Local
                                                                           MYHL HUMAN.
P13535; Q14910;
Ol-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, KELETAL MUSCLE, PERINATAL
       TISSUE-Skeletal muscle;
MEDLINE-90323631; PubMed-2373371;
Karsch-Mizrachi I., Feghali R., S
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
MOD_RES
MOD_RES
CONFLICT
CONFLICT
SEQUENCE
                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                        MYH8_HUMAN
P13535; Q1
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                                  SEQUENCE
                                                NCBI_TaxID=9606
                                                                          HOMO
  Generation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00193; MYOSINHEAVY ProDom; PD000355; myosin_head
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                                                                         sapiens (Human)
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                                                                                                                                                                                                           TSEIQDALDACNAKIVALENARSRLT----AEADANRL-----
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PF01576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00242; MYSc;
                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                    -LEKKQKAFDKVIDEWKKKVDDLYLELDGAQRDARQLSGEAHKLRGQHDTL----;
  of a
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856
174
668
773
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Myosin_tail;
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 full-length
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690
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125
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                                                                                                                                                                                                                                                                                                                                                                                             61;
 human
                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
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M -> I (IN REF. 2).
MW; 6D65AE99BD013627 CRC64;
                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
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ALKYLATION
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ATP (BY SIMILARITY).
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        Shows T.B.
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
  perinatal
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(SH-1).
(SH-2).
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         Jr.,
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 myosin
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                                                                                       (MYHC-PERINATAL).
         Leinwand L.
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RA ESSET K., Tidhar A., Myszkowski M.;

RY TISOLation and characterization of the human perinatal MHC promoter.";

RI Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

CC :- FUNCTION: MUSCLE CONTRACTION.

CC :- SUBUNIT: MUSCLE CONTRACTION.

CC :- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC :- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

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SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
MEDLINE=95324556; PubMed=7601129;
Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman
stedman H.H., Rubinstein N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Reghali R., Leinwand L.A.;
"Molecular genetic characterization o
human perinatal myosin heavy chain.";
J. Cell Biol. 108:1791-1797(1989).
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Gene 89:289-294(1990).
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SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD SIMILARITY: CONTAINS 1 IQ DOMAIN.
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                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                  Swiss Institute of Bioinformatics and the
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Pfam; Pfam; EMBL; EMBL; EMBL; EMBL; entities or send a Pfam; PIR; A30220; A30220 HSSP; P13538; 2MYS. MIM; 160741; the between European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed. ; M36769; AAC17185.1; ; Z38133; CAA86293.1; ; X51592; CAA35941.1; ; M35250; AAA36346.1; PF01576; PF00612; AF067143; AAC21557.1; PD000355; s requires a license agreement (See http://www.isb-sib.ch/announce/ an email to license@isb-sib.ch). IPR000048; IPR002928; IPR001609; myosin_head;
Myosin_tail; IQ; MYOSINHEAVY Myosin_tail. myosin_head. There are no rest Usage bу and for 5

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SMART; SM00242; MYSC; 1.
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K -> Q (IN REF. 1)
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-> H (IN REF. 2).
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-I- SUBUNIT: MUSCLE MYOSIAN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MIC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-I- SUBCELULIAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
-I- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEDTAPETIDES, CHARACTERISTIC FOR ALPHA-HELICAL COULED COILE.
-I- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-I- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
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"Protein structural domains in the Caenorhabditis elegans unc-54 myosin heavy chain gene are not separated by introns.";
Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
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InterPro; IPR001609; myosin_
Pfam; PF00063; myosin_head;
Pfam; PF01576; Myosin_tail;
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EMBL; V01494; CAA24738.1;
PIR; A02992; MWKW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  match cross-bridge spacings Nature 299:226-231(1982).
                                                                                                                                                                                             Myosin; Muscle procesu, carp-binding; Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                  Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                    Alkylation; Multigene family.
MYOSIN HEAD-LIKE.
COILED COIL (POTENTIAL).
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LIGHT MEROMYOSIN (LMM) ATP (BY SIMILARITY). ACTIN-BINDING. ACTIN-BINDING.
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                                                                                                                                 TISSUE-Keratinocytes;
MEDLINE-94357926; PubMed-8077230;
Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
"Cloning of the LamA3 gene encoding the alpha 3 chail ligand epiligrin. Expression in wound repair.";
J. Biol. Chem. 269:22779-22787(1994).
                                            Uitto J.,
                                                           Vidal F., Baudoin
                      "Cloning
                                                                               SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS MEDLINE=96163880; PubMed=8586427;
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Mammalia; Eutheria; Primates;
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, Baudoin C., Miquel C., Galliano
, Ortonne J.-P., Meneguzzi G.;
of the laminin alpha 3 chain gene
ozygous deletion in a patient with
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ALKYLATION (SH-1).
ALKYLATION (SH-2).
E -> R (IN REF. 2).
I -> L (IN REF. 2).
MW; B66F0BB2FE27B67F CRC64;
                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
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(LAMA3)
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ORGANIZATION INTERACTING
            OF.
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KERATINOCYTES (1) CELL ADHESION D INTEGRIN ALPHA-ION VIA TYROSINE

COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH EN THE ALPHA-3 CHAIN IS A SUBURIT OF LAMININ-5 (EPILIGRIN/KALININ/NICEIN), AND POSSIBLY ALSO A COMPONENT OF LAMININ-6 (K-LAMININ) AND LAMININ-7 (KS-LAMININ). COMPONENT OF LAMININ-7 (KS-LAMININ) IN THE BASEMENT SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT). SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTIN DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WITO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED CONSISTING OF THREE SAMMA), WHICH ARE BO END

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-THE SEQUENCE SHOWN HERE TWO ISOFORMS A AND B DI DIFFER IN THEIR N-HE SMALLER VARIANT

EPITHELIA AND IN OTHER SPECIALIZED TISSUES WITH PROMINENT SECRETORY OR PROTECTIVE FUNCTIONS. EPITHELIAL BASEMENT MED AND EPITHELIAL CELL TONGUE THAT MIGRATES INTO A WOUND BED DIFFERENTIAL AND FOCAL EXPRESSION OF THE ALPHA-3 CHAIN IS TISSUE SPECIFICITY: SKIN; RESPIRATORY, URINARY, AND DIGESTIVE MEMBRANE OBSERVED

-

INDICTION: LAMININ-5 IS UP-REGULATED IN WOUND SITES OF HUMAN SKIN. DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

DOMAIN: DOMAIN G IS GLOBULAR.

DISEASE: DEFECTS IN LAMA3 ARE A CAUSE OF JUNCTIONAL EPIDERMOLYSIS BULLOSA (JEB) GRAVIS, ALSO KNOWN AS HEBLITZ TYPE JEB. IT IS A BLISTERING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION OF BASAL CELLS FROM THE BASEMENT MEMBRANE DUE TO A DECREASED NUMBER OF HEMIDESMOSOMES. LAMININ-5 IS MISSING FROM THE BASEMENT MEMBRANE OF PATIENTS WITH THE GRAVIS FORM ę EPIDERMOLYSIS

SIMILARITY: SIMILARITY: CONTAINS 2.5 LAMININ EGF-LIKE DOMAINS.
5 LAMININ G-LIKE DOMAINS.

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Glycoprotein; Basement membrane; Extracellular matrix; Laminin EGF-like domain; Cell adhesion; Repeat; Signal Alternative splicing; Epidermolysis bullosa. SMART; SMART; PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01248; LAMININ_TYPE_EGF; Pfam; EMBL; EMBL; SIGNAL Pfam; InterPro; IPR000561; InterPro; IPR002049; InterPro; IPR001791; InterPro; MIM; 226700; (T; SM00180; EGF_Lam; (T; SM00180; EGF_Lam; (T; SM00282; LamG; 5. NT; SM00210; TSPN; 1. ; L34155; AAA59483.1; X85107; CAA59428.1; X85108; CAA59429.1; P02468; ITLE. PF00053; IPR003129; splicing; ; laminin_EGF; 2. ; laminin_G; 2. 0; EGF_Lam; 2. TSPN Laminin_EGF. Laminin_G. EGF-like Coiled

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LVRCAVDAATAYENILNAIKAAEDAANRAASASES
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LAMININ G-LIKE 2.

LAMININ G-LIKE 3.

LAMININ G-LIKE 4.

LAMININ G-LIKE 4.

LAMININ G-LIKE 5.

COILED COIL (POTENTIAL).

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EXAMININ G-LIKE 5.

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BY SIMILARITY.

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W -> R (IN REF. 2).
ATG -> GMC (IN REF. 2).
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R -> L (IN REF. 2).
E -> Q (IN REF. 2).
D -> A (IN REF. 2).
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G -> A (IN REF. 2).
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Pred. No. 1.7;
71; Mismatches
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LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 3. (INCOMPLETE).
DOMAIN II AND I (HEPTAT REPEATS).
5 X LAMININ G-LIKE REPEATS (DOMAIN G).
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2.5 X LAMININ EGF-LIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE-92315338; PubMed-1617731;
Galinski M.R., Medina C.C., Ingravallo P
Galinski m.r., Meding protein complex
                                                                          1141
                                                                                                                                                                                                                                                                                               EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium vivax (strain Belem).
Eukaryota; Alveolata; Apicomplexa;
NCBI_TaxID-31273;
                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Q00798;
                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: INVOLVED IN RETICULOCYTE HUMAN RETICULOCYTE CELLS.
-i- SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 69:1213-1226(1992)
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143 ILKANAAGKDK--GVEELEKLSGSL----ESLSKAAKEMLANSVKELTSPVVHGNNSGKD
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                                               AYTISTLITQKLSKLNGS-EGLKEKIAAAKKCSEEFSTKLKDNHAQLGIQGVTDENAKKA
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P36956; 1AM9.
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BINDING PROTEIN 1 PRECURSOR.
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CYTOPLASMIC.
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CELL ATTACHMENT SITE (
CELL ATTACHMENT SITE)
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RETICULOCYTE
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Search completed: March 18, 2002, 10:11:52 Job time: 970 sec

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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                          Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borr
NCBI_TaxID=139;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=OC2;
                                                                                                                                    SEQUENCE
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Spirochaetaceae; Borrelia

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Query Match
Best Local S
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             121 KLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSV 180
                                                                                                                                                          A Match 49.9%; Local Similarity 98.9%; nes 186; Conservative
                                                                                                       GKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFST 120
KLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSV
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Pred. No. 2.8e-33;
2; Mismatches 0
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194 194 AA;

194 20452 MW; 712A6C5B7873C21F CRC64;

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01-NOV-1996 (TremBirel. 01, Lr
01-NOV-1996 (TremBirel. 17, Lr
01-JUN-2001 (TremBirel. 17, Lr
STRAIN=OC10;
Wang I.-N., Dykhuizen D.E.,
Submitted (OCT-1997) to the
EMBL; AF029869; AAB86552.1;
                                                                                                                                                                                                                                            Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; s
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01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
OUTER SURFACE PROTEIN C (FRAGMENT).
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                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                   NCBI_TaxID=139;
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Jauris-Heipke S., Liegl G., Preac-Mursic V., Roessler D., Schwab E Soutschek E., Will G., Wilske B.;

"Molecular analysis of genes encoding outer surface protein C (Osp evidence of lateral gene exchange of ospC.";

J. Clin. Microbiol. 33:1860-1866(1995).

EMBL; X81522; CAA57242.1;

InterPro; IPR01800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

SEQUENCE 211 AA; 22214 MW; BFE8C7820CDE10D3 CRC64;
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Bacteria; Spirochaeta
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ales; Spirochaetaceae; Borrelia.
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Spirochaetaceae; Bor
                 Dunn J.J., Luft B.J.;
EMBL/GenBank/DDBJ databases.
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Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
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01-MAY-1997 (TrEMBLrel. 03, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
OUTER SURFACE PROTEIN C (FRAGMENT).
OSPC.
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Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

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SEQUENCE 191 AA; 20502 MW; E4FB
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KDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSVKE
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L42868; AAB37011.1; -.
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193 AA;
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Spirochaetaceae; Bor
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Pred. No. 1.9e-32;
1; Mismatches 2;
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Mol. Microbiol. 18:257-269(1995).
EMBL; L42893 ABB37001.1;
Interpro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
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NCBI_TaxID=139;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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0UTER SURFACE PROTEIN C (FRAGMENT).
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  MEDLINE-95154673; PubMed-7851744; Stevenson B., Barthold S.W.;
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                                                NCBI_TaxID=139;
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Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
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EMBL; U04281; AAC43297.1; -.

InterPro; IPR001800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

SEQUENCE 210 AA; 22526 MW; 2D672991D584E4EE CR
                                                                                                                     InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
Signal; Lipoprotein; Outer membrane
SIGNAL 1 18
POTENT
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OUTER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrel
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J. Bacteriol. 177:3036-3044(1995).
EMBL; X84765; CAA59236.1; .
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Pfam; PF01441; Lipoprotein_6; 1.
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||||||||||
|GKKIKNDGSLGDEANHNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD001149; Lipoprotein_6; 1.
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178 #
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18724 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.9%;
99.4%;
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Spirochaetaceae; Bor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 849; DB 2
Pred. No. 6e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49A6F785145CC208 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                           130
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Q9AGB1
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Query Match
Best Local :
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Best Local
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Q9AGB1;
01-JUN-2001 (Tr
01-JUN-2001 (Tr
01-JUN-2001 (Tr
0SPC-MODIFIED.
                                                                                                                                                                       VARIANT
SEQUENCE
                                                                                                                                                                                                        Kumaran D., Eswaramoorthy S., Luft B.J., Ko. Lawson C.L., Swaminathan S.;
"Crystal structure of outer surface protein disease spirochete, Borrelia burgdorferi.",
EMBO J. 0.0-0(2001).
                                                                                                                                                                                                                                                                                                                                                          OSPC
                                                                                                                                                                                                                                                                          STRAIN-HB19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marti-Ras N., Postic D., Foretz M., Submitted (MAR-1997) to the EMBL/Ger EMBL; U91795; AAB81892.1; -. INTERPROTE INTERPROTEIN Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1. ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97478003; PubMed=9336916;
Ras N.M., Postic D., Foretz M., B.
"Borrelia burgdorferi sensu stric
U.S.A.'?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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MSGAYLISTLITKKISAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAK
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                                                                                                       161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162;
                                                                                                                                                                                  AF337548; AAK21289.1;
NT 61 61
                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                Spirochaetales;
                                                                                                                                                                       165
                                                                                                                                                                                                                                                                                                                                                                               1 (TremBirel. 17,
1 (TremBirel. 17,
1 (TremBirel. 17,
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174 AA;
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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18291 MW;
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17833
                                                                                                                43.4%;
98.2%;
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                                                                                                                                                                      MW;
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                                                                                                                                                                                                                                                                                                                             e disease spirochete).
Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foretz M., Baranton (
                                                                                                    2
                                                                                                    Score 786; DB Pred. No. 3.2e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M., Baran
stricto,
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••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 790; DB 2;
Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                     -> I.
56E01536D22F61BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A14F5B8BA151A278
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                                                                                                                                                                                                                                                                                                                                                                                                                                   165
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                                                                                                                  DB 2;
.2e-28;
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                                                                                                                              Length 165
                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
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                                                                                                                                                                                                                                                               Dunn J.J.,
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                                                                                                                                                                                                                                     Lyme
                                                                                                   Gaps
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RESULT ON THE PROPERTY OF THE 
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Best Local S
Matches 164
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O34121;
O34121;
O34121;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SUFFACE PROTEIN C (FRAGMENY).
Borrella burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrel
NCBL_TaxID-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marti-Ras N., Postic D., Foretz M., B
Submitted (MAR-1997) to the EMBL/GenB
EMBL; U91794, AABB1891.1; -
Interpro; IPRO01800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
Probom; PD001149; Lipoprotein_6; 1.
NON_TER 168 168
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031115;
031115;
01-JAN-1998
01-JAN-1998
01-JUN-2001
STRAIN-OC3;
Wang I.-N., Dykhuizen D.E.,
Submitted (OCT-1997) to the
EMBL; AF029862; AAB86545.1;
                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
00TER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97478003; PubMed-9336916;
Ras N.M., Postic D., Foretz M., Baranton G.;
"Borrelia burgdorferi sensu stricto, a bacterial
U.S.A.'?";
                                                                                                                                Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; SCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-TETS;
                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164;
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168 /
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ilarity 98.2%;
Conservative
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17704 MW;
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the EMBL/GenBank/DDBJ
                                                                                                                                                         s disease spirochete).
Spirochaetaceae; Born
    Dunn J.J., Luft B
EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 782; DB 2
Pred. No. 5e-28;
1; Mismatches
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Pfam; PF01441; Lipopro
ProDom; PD001149; Lipo
NON_TER 193 193
SEQUENCE 193 AA; 20
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NON_TER
SEQUENCE
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Submitted (OCT-1997) to the EMBL/Ger

EMBL; AF029871; AAB86554.1; -

InterPro: IPR001800; Lipoprotein_6.

ProDom; PD001149; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
OUTER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                                                       STRAIN-OC12;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     Bacteria; Spirochaetales; NCBI_TaxID=139;
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 VKELTSPVV
                               TKLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANS
                                                                          IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS
                                                                                                         ISCNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKA
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                      KKLEGEHAQI
                                                                IGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFT
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                                                                                                                                                             Similarity
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194 AA;
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                     LGIENVTDENAKKAILITDAA-KDKGAAELEKLFKAVENLAKAAKEMLANS
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20640
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79.8%;
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75.1%;
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                                                                                                                                                                                                                                                                                                                                                 s disease spiroch
Spirochaetaceae;
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                                                                                                                                                                                                                                                                                 Dunn J.J., Luft B
EMBL/GenBank/DDBJ
                                                                                                                                                   Score 664; DB 2;
Pred. No. 9.1e-23;
9; Mismatches 26;
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186

VKELTSPIV

034120

PRELIMINARY;

184 A.

Last sequence update)

update)

Borrelia

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RESULT 15
P94234
ID P94234
AC P94234
DT 01-MAY
DT 01-JUN
DE OUTER
GN OSPC.
OS BORTCEL
OC BACTER
OX NCBI_T
RN [1]
RP SEQUEN
RC STRAIN
RX MEDLIN
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Best Local Similarity
Matches 142; Conserv
SEQUENCE FROM N.A.
STRAIN-28354;
MEDLINE-96296448; PubMed-8709845;
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Marti-Ras N., Postic D., Foretz M., Baranton G.;

Marti-Ras N., Postic D., Foretz M., Baranton G.;

Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

EMBL: U91793; AABB1890.1; -.

InterPro; IPR001800; Lipoprotein_6.

Ffam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
01-JER SURFACE PROTEIN C (FRAGMENT).
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P94234;
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Ras N.M., Postic D., Foretz M., Baranton G.;
"Borrelia burgdorferi sensu stricto, a bacterial species 'made in U.S.A.'?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update
01-JUN-2001 (TrEMBLrel. 17, Last annotation update
01-JUN-2001 (TREMBLREL 17, Last annotation update
01-JUN-2001 (TREMBLREL 17, Last annotation update)
00-JUN-2001 (TREMBLREL 18, Last annotation update)
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia update updat
                                                                                                                                                     Borrelia burgdorferi (Lyme Bacteria; Spirochaetales;
                                                                                                                         NCBI_TaxID=139;
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 AA;
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19391 MW;
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Spirochaetaceae; Bor
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EMBL; L42895; AAB37003.1; -.
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                     Livey I., Gibbs C.P., Schuster R., "Evidence for lateral transfer and Lyme disease Borrelia.";
                                                                        182
                                                                                                                122
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                                                                                                                                 Local Similarity hes 142; Conserv
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                                                                      ELTSPVV
                                                                                           LEGEHAQLGIENVTDENAKKAILITDAA-KDKGAAELEKLFKAVENLAKAAKEMLANSVK 179
                                                                                                      LKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSVK 181
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193 AA;
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                                                                                                                                                                                                                             36.6%;
          18,
                                                                                                                                                                                                                                                                        20411 MW;
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; Pred. No. 1.1e-22;
17; Mismatches 26
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seq length:
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Match
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113:
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1: /SIDS8/gcgdata
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                                         WPI; 2001-050113/06.
N-PSDB; AAF29021.
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                                                                                                                                                                                                                                                                    standard; Protein;
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                                                                                                                                                                                                                                          vaccine; chimeric protein; tick.
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                            ospC;
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Borrelia
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86.6%; Pred. No. 1.1e
Live 20; Mismatches
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                            disease;
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                                       protein
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standard;

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Compositions of OspC polypeptides Lyme disease are used to immunize to Lyme disease -
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317; Conserv
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                           Mismatches
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nus. These may
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RESULT
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Best Local Similarity
Matches 311; Conserv
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Borrelia
vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease -  \begin{array}{c} \\ \\ \end{array} 
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Chimeric -
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DB; AAF29022.
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                   standard;
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24; Mismatches 31; I
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Lyme disease are used
to Lyme disease -
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DB; AAF29038.
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Borrelia
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Pred. No. 2e-8
25; Mismatches
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                                                                                                                                                                                                                                                                                              .J; DB 22;
2e-87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Luft
                                                                                                                                                                                                                                                                                            31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       s of Borrelia v
detect immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
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Best Local Similarity
Matches 310; Conserv
                                                                                                                                                                                                                                                           The present invention provides compositions comprising ospc proteins and chimeric ospc proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
                                                                                                                                                                                                                                                                                                                         Compositions of OspC p
Lyme disease are used
to Lyme disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200078966-A1
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Chimeric -
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                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                      Claim 43; Page 89; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                   Dattwyler RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-1999;
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                                                                                                                                                      Lyme
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                                                                                                                     KLKSEHAVLGLDNLTDDNAQRAILKKH-ANKDKGAAELEKLFKAVENLSKAAQDTLKNAV
                2001-050113/06
)B; AAF29018.
STEFTNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDT
                                                                                    klkdnhaqlg1qgvtdenakkailkanaagkdkgveeleklsgsleslskaakemlansv
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Borrelia
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                                                                                                                                                                                                                                                                                                                                polypeptides from strains of Borrelia which caus
d to immunize animals and detect immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease;
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                                                                                                                                                                                        Score 1479; DB 22;
Pred. No. 3e-87;
5; Mismatches 31;
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gkkikndgsldneanrnesllagaytistlitqklsklngseglkekiaaakkcseefst 143

Query Match Best Local S Matches 309

Match 82.1%; Score 1476; DB 22; Local Similarity 83.5%; Pred. No. 5.1e-87; hes 309; Conservative 26; Mismatches 31;

Length Indels

393; 4.

Gaps

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               The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads to Lyme disease.
                                                                                                                                                                                                                                                                        Chimeric -
Chimeric -
                                                                                               Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
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N-PSDB; AAF29036.
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                                                                                                                                                                                                                                                                                                                   Borrelia
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                                                                     Claim 43; Page 133-134; 160pp; English
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                                                                                                                                                      Dattwyler RJ,
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Sequence
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                                                                                        disease
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393 AA;
                                                                                                                                                                                                                                                                        Borrelia
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                                                                                                                                                                                                                                                                                                                  chimeric ospC protein
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                                                                                                                                                                                                  9908-0140042
                                                                                                                                                                                                                                                                                                 Lyme disease;
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                                                                                                                                                                                                                                                                                                                                                                         Protein;
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                                                                                                                                                      Dykhuizen
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                                                                                                                                                                                                                                                                                                   vaccine;
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                                                                                                                                                                                                                                                                                                                    ID NO:
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                                                                                                                                                      Luft
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                                                                                                                                                       'n,
                                                                                                                                                       Gomes-Solecki M;
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RESULT AAB62713
ID AAB6
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                                                                                                                                                                                                      Query Match
Best Local S
Matches 262
                                                                                                                                                                                                                                                                                                                                                                The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                 to Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
      120
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Chimeric -
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                                                                                                                                                                                                                           Local Similarity
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                                                                                                               KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK
                                   IGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTN 119
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DB; AAF29017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 86-87; 160pp;
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Borrelia
                                                                                                                                                                                                                                                                                                           377 AA;
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                                                                                                                                                                                                 Score 1225.5; DB 22; Length 377; Pred. No. 4.9e-71; 3; Mismatches 61; Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; tick.
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                                                                                                                                                                                               Gaps
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В Qy

Matches Query Match Best Local

Similarity

68.1%; 70.2%;

Conservative

42;

Score 1224; DB Pred. No. 6e-71; 2; Mismatches

22; 61;

373; 8;

Indels Length

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 Sequence
                  to Lyme
                           The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
                                                                                                   6
                                                                                                        Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                                                                                                                                                                                                                                                                                    Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                 Borrelia sp chimeric ospC
                                                                                Claim 43;
                                                                                                                                          N-PSDB;
                                                                                                                                                                       Dattwyler RJ,
                                                                                                                                                                                      (UYNY ) UNIV N
(BROO-) BROOK
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                                                                                       The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leaves the state of the spread by ticks and leaves the spread by tic
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The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ospC; Lyme
                                                                                                Page 94-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia
Borrelia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                              INC.
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                                                                                                                                                                                                                                                                        ВJ,
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Lyme disease.

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                                                                                            WPI; 200
N-PSDB;
                            Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                                                                                                                                                                     (UYNY )
(BROO-)
                                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Borrelia sp. Chimeric - Borrelia sp.
                                                                                                                                                 Dattwyler RJ,
                                                                                                                                                                                                                                          18-JUN-1999;
                                                                                                                                                                                                                                                                              19-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia; ospC; Lyme disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia sp chimeric ospC protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-2001
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DB; AAF29043.
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                                                                                                                                                                                 UNIV NEW YORK STATE RES FOUND. BROOK BIOTECHNOLOGIES INC.
                        disease
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61; Conservative
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و
                                                                                                                                               Dykhuizen
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Pred. No. 1.1e-70;
5; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 chimeric protein;
                                                                                                                                             Luft BJ,
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                                                                                                                                           Gomes-Solecki
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Best Local S
Matches 261
                 Dattwyler RJ,
                                                                                                                                             Chimeric -
Chimeric -
                                 (UYNY ) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
                                                                                                                                                                     Borrelia; ospC; Lyme disease; vaccine; chimeric protein;
                                                                                    19-JUN-2000; 2000WO-US16915
                                                                                                       28-DEC-2000.
                                                                                                                        WO200078966-A1
                                                                                                                                                                                           Borrelia sp
                                                                                                                                                                                                                03-APR-2001
                                                                 18-JUN-1999;
                                                                                                                                                                                                                                  ААВ62731;
                                                                                                                                                                                                                                                   AAB62731 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and learners.
                                                                                                                                                                                                                                                                                                      385
                                                                                                                                                                                                                                                                                                                                            325
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                                                                                                                                                                                                                                                                                                              LSKAAQDTLKNAVKEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 153; 160pp; English
                                                                                                                                            Borrelia
                                                                                                                                                      Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400 AA;
                                                                                                                                                                                           chimeric
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               Luft BJ,
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               Gomes-Solecki M;
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TELEPHONE: 617-861-6240
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 LKGYVLEGTLTAEKTTL--VVKEGT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 FK--AVENLSKAAQDTLKNAVKELT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 LVSKKVTSKDKSSTEEKFNEKGEVSEKII-----TRADGTRLEYTGIKSDGSGKAKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 -LKEKIDTAKQCSTE--FTNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 ATVDKLELKGTSDK--NNGSGYLEGVKADKSKVKLTIS-----DDLGQTTLEVFKEDGKT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 02173
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                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                  140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELTSPIVHGNNSRKDGNAST----NSADESVKGPNLTEISKKITESNAVVLAVKEVETLL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLKAKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGKKIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lexington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΜA
                                                                                                                                                                   212 amino acids
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Two Militia Drive
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                  Conservative
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                                                                                                                                        single
                            36.6%;
72.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methods for Diagnosing Early Lyme
                20;
                                                                                                                                                                                                                                                                    UCT93-05
                            Score 657.5;
Pred. No. 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith & Reynolds, P.C.
              Mismatches
             7.6e-45;
hes 29;
                                         DB 1;
                                         Length 212;
           ω,.
         Gaps
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                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1:
Patent No.
                                                                                                                                                                                                                                                                                      TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338
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APPLICATION NUMBER: U
FILING DATE: 01-11-93
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APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                          55
                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                                                                                          LENGTH:
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ELATKAIGKKIGNNG---LEANQ-SKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTA 110
                                                                                GKDGNASANSADESVKG-----PNLTEISKKITESNAVVLAVKEVET----LLASID 54
                                                    GSQKENDLNLEDSSKKSHQNAKQDLPAVTEDSVSLFNGNKIFVSKEKNSSGKYDLRATID 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKELTSPIVHGN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLKSEHAVLGLDN--LTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTEFTN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122, App
0. 624856
                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                            588 amino acids
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                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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V: 435
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                                                                                                                                        35.6%;
39.1%;
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                                                                                                                                                                                                                                                                                                                                                                          BNL93-28A
                                                                                                                       Score 640; DB 4;
Pred. No. 6.8e-43;
5; Mismatches 110
                                                                                                                                                    Length 588;
                                                                                                                   Indels 122;
                                                                                                                   Gaps
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QVELKGTSDK--NNGSGTLEGSKPDKSKVKLTVSADLNTVTLEAFDA-SNQKISSKV-TK

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US-08-235-836C-107; Sequence 107; Application US/08235836C; Patent No. 6248562; GENERAL INFORMATION:
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; MOLECULE TYPE: US-08-235-836C-107
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                                                                                                                                                                                                                       TELEFAX: (516) 282-3729 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-9
ATTORNEY/AGENT INFORMATION:
AND AND ASSESSMENT APPORTMENT OF THE PRIOR OF T
                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acid
                                                                                                                                                                                                                                                                                             TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS
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APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296
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                                                                                                                                                                                                                                                                                                                                                                      NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
                                                                     LENGTH: 466 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 11973
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                                  protein
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Query Match

35.5%;

Score 638.5;

DB 4;

Length 466;

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APPLICANT: Fuchs, Renate
APPLICANT: Motz, Manfred
APPLICANT: Motz, Manfred
APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.001US2
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 00/209,603
EARLIER FILING DATE: 1994-03-10
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER FILING DATE: 1990-12-22
EARLIER FILING DATE: 1990-12-22
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER FILING DATE: 1990-06-13
NUMBER: DE SEQ ID NOS: 16
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                                                                                                                                                                         ; ORGANISM: Borrelia
US-09-196-293-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/09196293 Patent No. 6183755
                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ
SEQ ID NO 15
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Matches 166; Conservative
                                                                                            Query Match
Best Local Similarity
                                                                         Matches
                                                                                                                                                                                                              LENGTH: 20
TYPE: PRT
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                  MACNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKA 60
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ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDEIAAKAIGKKIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAK
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                                                                         Conservative
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                                                                                                                                                                                          burgdorferi
                                                                                            34.7%; Score 623.5; DB 4 69.5%; Pred. No. 3.5e-42;
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                                                                         24; Mismatches
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                                                                                                              DB 4;
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US-08-158-353-3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORIEY/AGENT INFORMATION:
NAME: CAITOII, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UCT9
TELECHOMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPHONE: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Padula
                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
180 ELTSPIV 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C STREET: Two Militia Drive
                                            137
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                                                                                                                                                                     17 ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                        1 MACNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version
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                                                                                                                       IGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTN 119
                                       KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                        KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
                                                                                                    IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
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                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                     single
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Methods for Diagnosing Early
Disease
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                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                  Score 623.5; DB 1;
Pred. No. 3.6e-42;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS LENGTH: 210 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 11973
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Brookhaven National Laboratory
                                                              137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
197
                             180 ELTSPIV 186
                                                                            120 KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLEKAVENLSKAAQDTLKNAVK 179
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nes 129; Conserv
                                                                                                                                                                                NAME: Bogosian, Margaret REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 29-APR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Upton
STATE: NY
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ELTSPVV
                                                          KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                                                                                     IGKKIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
                                                                                                                                       IGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTN 119
                                                                                                                                                                                                                                                                                                                                                                           amino acid
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203
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                                                                                                                                                                                                                                                                                                                                              protein
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Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                               34.4%; Score 617.5; DB 4; 69.0%; Pred. No. 1.1e-41;
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                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                            Length
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RESULT 8 US-08-209-603E-15 ; Sequence 15, Application US/08209603E

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; PUBLICATION INFORMATION:
US-08-209-603E-15
                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                              Matches 129;
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                                                                                                                                                                                                                                                                                                                                                             HYPOTHLIANDE N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORTANISM: B. BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEPAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOF
COMPUTER: AT6T - IBM C
OPERATING SYSTEM: MS-C
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP90/02282
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/862,535
FILING DATE: 19-UN-1992
                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
TTRRARY: DSM 5662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS TITLE OF INVENTION: FROM BORRELIA BURGDORFERI NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                         LIBRARY: DSM 5662 POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
DESCRIPTION: PRO
HYPOTHETICAL: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-JUN-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
120 KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 99 PARI
                                                    77
                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: ROBINSON, WILLIAM R. REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 10-MAR-1994 CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                              TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                  IGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTN 119
                                                  IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN
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                                                                                                                                                                              Conservative
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CHECK, ERWIN
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                                                                                                                                                                                                                                                                                                                         N/N
                                                                                                                                                                                             34.3%; Score 616.5; DB 4 69.0%; Pred. No. 1.3e-41;
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                                                                                                                                                                                                                                                                          amino acid analysis
N/A
                                                                                                                                                                              24; Mismatches
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                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                            Length 210;
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US-08-031-295-2; Sequence 2, A

Application US/08031295

RESULT 10

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                                                                                                                                                                                                                                                         Matches 130;
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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 197
                178 VKELTSPIV 186
                                                                137 TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS 196
                                                                                118 TNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
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                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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CITY: Lexington
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                                                                                                                                               60 AIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTEF 117
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/158,353 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Hamilton, Brook, STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                                                                                            AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELTSPVV 203
VKELTSPVV 205
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                                                                                                                                                                                                                                                                                                                                                                          linear
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Methods
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                                                                                                                                                                                                                                                         Score 588.5; DB 1;
Pred. No. 2.1e-39;
0; Mismatches 36;
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                                                                                                                                                                                                                                                                                       Length 212;
                                                                                                                                                                                                                                                          Indels
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RESULT 11
US-07-903-580-2
; Sequence 2, Application US/07903580
; Patent No. 6221363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                 st Local Similarity tches 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                      178 VKELTSPIV 186
                                                                                                                                                                               137 TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: (FILING DATE: 22-JAN-: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/903,580
FILING DATE: 25-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                    197 VKELTSPVV 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LIVEY, IAN
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND COMPOSITION FOR
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                              77
                                                                                                                                                                                                                                                                       60 AIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNE-ELKEKIDTAKQCSTEF 117
                                                                                                                                                                                                                                                                                                                       17 ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 199303 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                          1 MACNNSGKDG-NASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                   AIGKKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDF 136
                                                                                                                                                                                                   TNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
CANT: LIVEY, Ian
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11-JUL-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                32.5%;
67.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Score 584.5; DB 1;
Pred. No. 4.3e-39;
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                                                                                                                                                                                                                                                                                                                                                                                               Indels 3;
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US-08-235-836C-34
Sequence 34, Application US/08235836C
Patent No. 6248562
GENERAL INFORMATION:
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                                                                                                                RESULT 12
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; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-07-903-580-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 11-JUL-1991
ATTORIEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,580
                                                                                                                                                                                        178 VKELTSPIV 186
                                                                                                                                                                                                                                           137
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FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                     197 VKELTSPVV 205
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APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND COMPOSITION FOR
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                                                                                                                                  77
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                                                                                                                                                                                                                                                                                                                                                                                                   1 MACNNSGKDG-NASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Alexandria
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                                                                                                                                                                                                                                   TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS 196
                                                                                                                                                                                                                                                                   TNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
                                                                                                                                                                                                                                                                                                       AIGKKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDF 136
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Dunn, John J.
Luft, Benjamin J.
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ilarity 67.2%;
Conservative 2
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Pred. No. 4.3e-39;
3; Mismatches 36;
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US-09-196-293-11
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Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                           Sequence 11, Application US/09196293 Patent No. 6183755
                                                                                                                                                                                            GENERAL INFORMATION:
        APPLICANT: Fuchs, Renate
APPLICANT: Motz, Manfred
APPLICANT: Motz, Manfred
APPLICANT: Soutscheck, Ervin
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
APPLICANT: NUVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorfer1
FILE REFERENCE: 738,001US2
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
APPLICATION NUMBER: 011-93
CURRENT APPLICATION NUMBER: US/09/196,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MATGARET C.
REGISTRATION NUMBER: 25,324
REFERENCE/POCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                           197 VKELTSPVV 205
                                                                                                                                                                                                                                                                                                                                                                                   178 VKELTSPIV 186
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                             TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.5%; Score 583.5; DB 4; Length 212; 68.3%; Pred. No. 5.1e-39; tive 21; Mismatches 36; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 6248562el Chimeric Proteins Comprising
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; SEQ ID NO 11
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-09-196-293-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER FILING DATE: 1994-03-10
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1990-12-21
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER TILING DATE: 1990-06-13
NUMBER OF SEQ ID NOS: 16
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SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,603E
FILING DATE: 10-MAR-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP90/02282
FILING DATE: 21-DEC-1990
                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FUCHS, RENATE
APPLICANT: WILSKE, BETTINA
APPLICANT: PREAC-WURSIC, VERA
APPLICANT: MOTZ, MANFRED
APPLICANT: SOUTSCHECK, ERWIN
                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS TITLE OF INVENTION: FROM BORRELIA BURGDORFERI NUMBER OF SEQUENCES: 15
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CITY: NEW YORK
STATE: NY
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                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                       MS-DOS Version
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Pred. No. 1.3e-38;
""Amatches 38;
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APPLICATION NUMBER: US 0 FILING DATE: 19-JUN-1992 ATTORNEY/AGENT INFORMATION:

US 07/862,535

REGISTRATION NUMBER:

ROBINSON, WILLIAM R.
RATION NUMBER: 27,224

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US-08-235-836C-36
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; ORIGINAL SOURCE:
US-08-209-603E-11
                                                                                                                                                                                                                                              Sequence 36, Application US/08235836C Patent No. 6248562 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: LKR-9217-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION: PROTEIN
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                 APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brookhaven National Laboratory
                                                   CITY: Upton
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
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                                        COUNTRY: U
ZIP: 11973
                                                                                                          STREET:
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Search completed: March 18, 2002, 09:55:35 Job time: 348 sec

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                                                                                                                                                                                                                                Query Match 31.3
Best Local Similarity 62.6
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (516) 282-372;
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET MUMBER: BNL9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
TELEPAX: (516) 282-3729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 01-11-93 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                         134
194 ELTNPVV
                           180 ELTSPIV 186
                                                                                      120
                                                                                                                 74
                                                                                                                          61 IGKKIGNNG-LEANQSKNTSILSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEETN 119
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                                                                                                                                                                  LENGTH:
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                                                   IGKKIKNDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSEKFTT 133
                                                                                                                                                                                                                                                                                                                                                 amino acids
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; Pred. No. 2e-37; 
34; Mismatches 32; Indels
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                 Score
                                                                                                                                                    1797
1797
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Match
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
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Gapop 10.0 , Gapext 0.5
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164.485 Million cell updates/sec
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US-09-596-746A-76
US-09-596-746A-76
US-09-596-746A-42
US-09-596-746A-42
US-09-596-746A-74
US-09-596-746A-74
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19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19
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equence 78,	e 56, App	equence 56,	e 52,	e 52,	64,	64,	80,	equence 80,	34,	60,	60,	24,	34,	28,	28,	24,	66, App		82,	82,	36,	62,	62,	26,	Sequence 36, Appl	30,	30,	26,	, 89	, 89	,2	72,	7	32,	Sequence 40, Appl

ALIGNMENTS

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; TYPE: PRT
; ORATNISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OSPC Chimera
US-09-596-746-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-596-746-38
                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Wi
SEQ ID NO 38
LENGTH: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/09596746
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
    Matches 368;
                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme DI FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes Solecki
    Conservative
                                                                                                                                                                                                                                                for Windows Version 4.0
100.0%; So 100.0%; Po vative 0;
Score 1797; DB 19;
Pred. No. 1.4e-124;
Prematches 0;
    Indels
                                        Length 368;
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    0.
    Gaps
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OTHER INFORMATION: OSPC Chimera
US-09-596-746A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-09-596-746A-38
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                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 368; Conserv
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SEQ ID NO 38
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 38, Application US/09596746A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 199-06-18
NUMBER OF SEQ ID NOS: 84
SOFTMARE: PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D:
FILE REFERENCE: 2631,1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
                                                                                                                                                                                                                                                                            LENGTH: 368
TYPE: PRT
ORGANISM: Artificial Sequence
181 LTSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDE
                                                                     121
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                                    IKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE
                                                                                                                                   IGKKIGNNGLEANOSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKOCSTEFTNK 120
                                                                                     IGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNK
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                                                                                                                                                                                         Conservative
                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                       Score 1797; DB 19;
Pred. No. 1.4e-124;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                       Cause Lyme Disease in Humans
                                                                                                                                                                                                            Length 368;
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US/09/596,746
PRIOR PELLING DATE: 2000-06-16
PRIOR ELLING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 76
LENGTH: 391
TYPE: PRT
ORGANITOR
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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385
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                                    ATKAIGKKIGNNGLEANOSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTE 301
                                                                                                                      TSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDEL 241
AVKELTS 391
                                                                              ATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTE
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                                                                                                                                                                                                                                                                                               Score 1789; DB 19; Pred. No. 6.1e-124;
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Dise;
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT ETLING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
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; ORGANISM: OSPC Chimera
US-09-596-746A-76
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Best Local S
Matches 366
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GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
                                                                                                                                                                                                                                       Sequence 42, Application US/09596746A GENERAL INFORMATION:
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EQ ID NO 76
LENGTH: 392
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CURRENT APPLICATION NUMBER: US/09/596,746A

CURRENT FILING DATE: 2000-06-19

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 84
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99.7%; Pred. No. 6.1e-124;
tive 1; Mismatches 0; Indels 0
                                                                                         Disease
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APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CUGRENT APPLICATION NUMBER: US/09/596,746
CUGRENT FILING DATE: 200-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FrastSEQ for Windows Version 4.0
SEQ ID NO 42
LENGTH: 367
TYPE: PRT
OPCRANTSM: Artificial Sequence
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; OTHER INFORMATION: OSPC Chimera US-09-596-746A-42
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Best Local Similarity
Matches 319; Conserv
OTHER INFORMATION: OSpC -09-596-746-42
                              FEATURE:
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86.7%;
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Pred. No. 2.1e-105;
20; Mismatches 27;
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Best Loc Matches

Local

al Similarity 318; Conserv

Conservative

86.6%;

Pred. No. 4.9e-105; 0; Mismatches 27;

Indels

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US-09-596-746-74
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Best Local S
Matches 317
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EQ ID NO 74
LENGTH: 391
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FASTSEQ for Windows Version 4.0
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APPLICANT:
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  145
           122 KSEHAVLGLDNUTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKEL 181
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Seinost, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                            Luft, Benjamin J.
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                                                                                                                                                    85.1%; Score 1530; DB 19;
86.4%; Pred. No. 8.9e-105;
tive 21; Mismatches 27;
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                                                                                                                                                                             Length
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; SOFTWARE: FastSE
; SEQ ID NO 74
; LENGTH: 392
; TYPE: PRT
; ORGANISM: OSPC C
US-09-596-746A-74
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US-09-596-746A-74
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Matches 317; Conservat
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Haria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D.
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                                                                                                                                                         ANSVKEL
                                                                                                                    ATKAIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCS 299
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                       KNAVKEL
                                                                   TEFTNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTL
                                                                                                      ATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCS
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86.4%;
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erald
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Pred. No. 8.9e-105;
1; Mismatches 27;
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APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Dathwyler, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrella burgdorferi and
TITLE OF INVENTION: Borrella afzelii That Cause Lyme Disease in Humans
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LEUNGH: Artificial Sequence
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US-09-596-746-40
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                                                                                                                                    Sequence 40, Application US/09596746 GENERAL INFORMATION:
                                    APPLICANT: Dattwyler, Raymond J. APPLICANT: Seinost, Gerald APPLICANT: Dykhuizen, Danial APPLICANT: Luft, Benjamin J. APPLICANT: Maria J.C. Gomes-Sole
    TITLE
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    OF INVENTION:
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C. Gomes-Solecki
Groups of Borrelia burgdorferi and
Borrelia afzelii That Cause Lyme D
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US-09-596-746A-32; Sequence 32, Application US/09596746A; GENERAL INFORMATION:
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; OTHER INFORMATION: OspC Chimera
US-09-596-746-40
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
                                                                   CURRENT APPLICATION NUMBER: US/09/596,746A CURRENT FILING DATE: 2000-06-19 PRIOR APPLICATION NUMBER: US 60/140,042 PRIOR FILING DATE: 1999-06-18 NUMBER OF SEQ ID NOS: 84 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 32 LENGTH: 370
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Best Local
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APPLICANT:
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                   LENGTH: 370
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
OTHER INFORMATION: OspC Chimera
                 FEATURE:
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Maria J.C. Gomes-Solecki
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                                                                                                                                                                                                                                                                                                              Dykhuizen, Danial
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Pred. No. 1.6e-101;
14; Mismatches 31;
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US-09-596-746A-32

Query Match 82.t Best Local Similarity 83.8 Matches 311; Conservative

82.6%; Score 1484; DB 19; 83.8%; Pred. No. 2.1e-101; tive 25; Mismatches 31;

Length 370; Indels 4;

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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT ETLING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH: 392
TYPP: NOW
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US-09-596-746-72
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Best Local
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APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
FILE REFERENCE: 2631.1002-001
        85
                                                                                                                     Local Similarity hes 310; Conserv
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                                                      GKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKL
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                                                                                                               82.5%; Score 1482.5; DB 19
84.0%; Pred. No. 2.9e-101;
vative 25; Mismatches 31;
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; ORGANISM: OSPC Chimera
US-09-596-746A-72
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SOFTWARE: FastSEQ for
SEQ ID NO 72
LENGTH: 393
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APPLICANT: Dattwyler, Raymond J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
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                 300 TEFTNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTL 359
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                                                                       242 ATKAIGKKIGNN-GLEANQSKNTSLLSGAYAISDLIAEKLNVLKNE-ELKEKIDTAKQCS 299
                                                                                                                      206 TSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLTSIDEL
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A-KAIGKKIKNDYSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCS
                                                                                                                                      TSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDEL
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Seinost, Gerald
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US-09-596-746-68
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 369
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Best Local Similarity
Matches 310; Conserva
                                         Sequence 68, Application US/09596746 GENERAL INFORMATION:
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APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT:
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Dattwyler, Raymond J.
Seinost, Gerald
Dykhuizen, Danial
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83.8%; Pred. No. 4.9e-101;
htive 25; Mismatches 31;
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SEQ ID NO 68
LENGTH: 393
TYPE: PRT
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Best Local Similarity
Matches 309; Conserv
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APPLICANT: Maria J.C. Gomes Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION UMBER: US 60/140,042
PRIOR PILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
UMBER OF SEQ ID NOS: 84
359 LKNAVKELTS:
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83.5%; Pred. No. 8.9e-101;
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4

Search completed: March Job time: 973 sec 18, 2002, 10:08:45

GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

Compugen Ltd

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Minimum DB seq
Maximum DB seq
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1: /cgn2_6/ptcdata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/US10_NEW_COMB.pep:*

8: /cgn2_6/ptcdata/2/paa/US10_NEW_COMB.pep:*
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290.158 Million cell updates/sec
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Sequence 5883, Ap
Sequence 13080, A
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Sequence 15590, A
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Sequence 1515, Ap
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Sequence 15045, Ap
Sequence 15045, A
Sequence 15046, A
Sequence 15045, A
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ALIGNMENTS

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APPLICANT: Mathiesen, Marianne J.
APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
NUMBER OF SEQ ID NOS: 40
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TYPE: PRT
; ORGANISM: Borrelia afzelii
US-09-974-992-7
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US-09-974-992-7
Sequence 7, Application US/09974992
GENERAL INFORMATION:
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Best Local S
Matches 130
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 197
                                 178 VKELTSPIV 186
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                                                                                                                                        y Match 32.7%; Score 588.5; DB 6;
Local Similarity 68.8%; Pred. No. 2.9e-32;
hes 130; Conservative 20; Mismatches 36;
                                                                                       TNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
                                                                     TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS
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US-09-974-992-5

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; ORGANISM: Borrelia garinii
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     Query Match
Best Local Similarity
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PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
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Best Local
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TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
CURRENT FILING DATE: 2001-10-10
CURRENT FILING DATE: 2001-10-10
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                                                                                                                              LENGTH: 20
TYPE: PRT
                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/180,089 PRIOR FILING DATE: 1999-05-13
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mathiesen, Marianne J.
APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09974992 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE 459-666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/DK97/00203 PRIOR FILING DATE: 1997-05-02 NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
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TYPE: PRT
ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mathiesen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 NSVKELTSPVV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 32.4%; Score 583; DB 6; Local Similarity 67.5%; Pred. No. 6.8e-32; Pres 129; Conservative 24; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSTKLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTNKLKSEHAVLGLDNLTDDNAQRAILKKH-ANKDKGAAELEKLFKAVENLSKAAQDTLK 175
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                                                                                                                                                207
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         Conservative
                   31.6%;
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   33;
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Score 567; DB b; L
Pred. No. 7.6e-31;
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                                    Length 207;
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SEQ ID NO 5883
LENGTH: 837
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Best Local ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2001-0
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PRIOR FILING DATE: 2000-05-26
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TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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218 AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN 272
                                   110 AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE 164
                                                                                                                                                  100 NHNLEVAKQNANTAIDGLTSLNGPQKAKLKEQVGQATTLPNVQTVRDNAQTLNTAMKGLR 159
                                                                                  160
                                                                                                            54 DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE----KLNVLKNEELKEKIDT 109
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                                                                                                                                                                                     4 NNSGKDGNASANSADE---SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI---- 53
                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IGKKIGNNG-LEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTN 119
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                                                                          DSIANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
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Zyskind, Judith W.
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                                                                                                                                                                                                                                  Conservative
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Pred. No. 3.8e-05;
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5883
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Best Local
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APPLICANT:
APPLICANT:
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TYPE: PRT
ORGANISM: Staphylococcus aureus
10-072-851-5883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITERA.028A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Carr, Grant J.
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                     223
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                                                                                                                                                                                                                            54 DELATKAIGKKIGNNGLEANOSKNTSLLSGAYAISDLIAE----KLNVLKNEELKEKIDT
                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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 AVVLAVKEVETLL-----ASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDL | | | : | : : | :::|
                                                                                                                      AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN
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                                                    NADALNTAMTNLKNGIQD-----QNTIKQG-VNFTDADEA---
                                                                        NLS--KAAQDTLKNAVKELTSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESN
                                                                                                                                                         AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE
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Ohlsen, Kari L.
Zyskind, Judith W.
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Yamamoto, Robert
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Zamudio, Carlos
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US-09-815-242-13080
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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SEQ ID NO 13080
                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/815, CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/191,078
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TYPE: PRT
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                                                                                                                                                                                                                                                                                              4 NNSGKDGNASANSADE----SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI----
AVVLAVKEVETLL-----ASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDL | | | : | : | : : | : : : | : : : |
                                                   NADALNTAMTNLKNGIQD-----QNTIKQG-VNFTDADEA-----
                                                                        NLS--KAAQDTLKNAVKELTSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESN 222
                                                                                                                                                         AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE
                                                                                                                                                                                           DSTANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
                                                                                                                                                                                                                                                             NHNLEVAKQNANTAIDGLTSLNGPQKAKLKEQVGQATTLPNVQTVRDNAQTLNTAMKGLR 196
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                                                                                                                      AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI----EGATHVNEVTQAQN
                                                                                                                                                                                                                                                                                                                                    91;
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Trawick, John D.
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Zyskind, Judith W.
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Pred. No.
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APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying the
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 50/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13080
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Best Local Similarity
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APPLICANT:
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TYPE: PRT
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   407 TS--INNAQKEALKSQIEGATTVÄGVNQVSTTASELNTAMSN------LQNGINDE
                                                                                                                                                                                                                                                                                                                                        54 DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE ---- KLNVLKNEELKEKIDT 109
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                                       IAEKLNVLKNEELKEKID------TAKQCSTEFTNKLKSEHAVLGLDN-LTDD
                                                                            AYTNAVTQAEQILNKAQGPNTSKDGVETALENVQRAKNELNGNQNVANAKTTAKNALNNL
                                                                                                              AVVLAVKEVETLL-----ASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDL
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Zyskind, Judith W.
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Zamudio, Carlos
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ
SEQ ID NO 5835
LENGTH: 2434
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                           762 DSIANEAT-IKAGONYTDASONKOTDYNSAVTAAKAIIGOTTSPSMNAQEINQAKDOV-T
       998 VSTTASELNTAMSNLONGINDEAATKAAOKY----TDADREKOTAYNDAVTAAKTLLDK 1052
                                           224 VYLAVKEVETLLASI-----DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLI--
                                                                                                                                                                                          158 KLFKAVENLSKAAQD--TLK-------------NAVKELTSPI--VHGNNSRKD-- 194
                                                                                                                                                                                                                                                                                                                                            54 DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE----KLNVLKNEELKEKIDT 109
                                                                                                                                                                                                                                                                                                                                                                                                                     4 NNSGKDGNASANSADE----SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI----
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                                                                              ETALENVQRAKNELNGNQNVANAKTTAKNALNNLTSINNAQKEALKSQIEGATTVAGVNQ
                                                                                                                                                       ALNTAMTNIKNGIODONTIKOGVNFTDADEAKRNAYTNAVTQAEQIINKAQGPNTSKDGV 937
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09815242
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                                                                                                                      -GNASTNSADESVKGP--NLTEISKKITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                            81; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 182; DB 6;
Pred. No. 0.00057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 132;
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RESULT 9
US-10-072-851-5835
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 5835
LENGTH: 2434
TYPE: PRT
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dest Local Similarity 22.2
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bussey, Howard TITLE OF INVENTION: Methods for Identifying TITLE OF INVENTION: Proliferation FILE REFERENCE: ELITRA.028A CURRENT APPLICATION NUMBER: US/10/072,851 CURRENT FILING DATE: 2002-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                            4 NNSGKDGNASANSADE---SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI---- 53
KLFKAVENLSKAAQD--TLK--------NAVKELTSPI--VHGNNSRKD--
                                                                                                                                                                                                                                                                       AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKK-----HANK-DKGAAELE
                                                                                                                                                                                                                                                                                                                 DSIANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
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                                                                ETALENVQRAKNELNGNQNVANAKTTAKNALNNLTSINNAQKEALKSQIEGATTVAGVNQ
                                                                                                                                                   ALNTAMTNIKNGIQDQNTIKQGVNFTDADEAKRNAYTNAVTQAEQILNKAQGPNTSKDGV
                                                                                                                                                                                                                                 AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQIEGATHVNEVTQAQNNAD
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Boone, Charles
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Yamamoto, Robert T.
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Zyskind, Judith W.
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Zamudio, Carlos
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22.2%;
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Pred. No. 0.00057;
31; Mismatches 161
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US-09-815-242-12996
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                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Staphylococcus
US-09-815-242-12996
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SEQ ID NO 12996
LENGTH: 6281
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                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26
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                                                                1599 AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQIEGATHVNEVTQAQNNAD 1656
                                                                                                                                                1541 DSIANEAT-IKAGONYTDASONKOTDYNSAVTAAKAIIGOTTSPSMNAQEINQAKDOV-T
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  158 KLFKAVENLSKAAQD--TLK------
                                                                                                          110 AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKK------HANK-DKGAAELE
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                                                                                                                                                                                       54 DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE ----KLNVLKNEELKEKIDT 109
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Zyskind, Judith W.
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Pred. No. 0.0019;
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                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 107; Conserv
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TITLE OF INVENTION: Methods for Identifying the
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/257,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF CEO TO NO.
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CURRENT FILING DATE: 2002-02-08
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                                                                                                          1541 DSIANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
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                                                                    110 AKQCSTEFTNKLK-----SEHAVIGLDNLTDDNAQRAILKK-----HANK-DKGAAELE 157
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Boone, Charles
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Yamamoto, Robert T
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Zyskind, Judith W.
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Zamudio, Carlos
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; Pred. No. 0.0019;
81; Mismatches 161; Indels 13
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SEQ ID NO 7646
LENGTH: 1881
TYPE: PRT
ORGANISM: Candida albicans
FERGURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1881)...(1881)
OTHER INFORMATION: X=any amino acid
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Best Local Similarity
Matches 112; Conserv
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TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
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CURRENT FILING DATE: 2001-12-20
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APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
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                                                                                                                  --ANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKELTSPIVHGNNSRKDGNASTNS---
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                                      ---ADESVKGPNLTEISKKITESNAVVLAVKEVETL----LASIDELA 242
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LOCATION: (1881)..(1881)

OTHER INFORMATION: X=any amino acid

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Best Local :
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LENGTH: 1881
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PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                     --ANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKELTSPIVHGNNSRKDGNASTNS--- 201
                                                                                                       SKE-ITTHNEQKT----SLKQDIAKLSQDHESAQTQLEDKENQLKELKASLEKHNTESAT 1629
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Yamamoto, Robert T.
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Zyskind, Judith W.
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Zamudio, Carlos
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--ADESVKGPNLTEISKKITESNAVVLAVKEVETL----LASIDELA 242
                                                                                                                                                                                                                                                                                                                              55; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                               DB 7;
                                                                                                                                                                                                                                                                                                                                                                Length 1881
                                                                                                                                                                                                                                                                                                                             Indels 121;
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                           146
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; ORGANISM: Staphylococcus aureus US-09-815-242-5815
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CURRENT ETLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILLING DATE: 2000-03-21
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/2042,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILLING DATE: 2000-10-23
PRIOR PPLICATION NUMBER: 60/253,625
PRIOR PRIOR PRIOR DATE: 2000-11-27
PRIOR PRIOR PRIOR DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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SEQ ID NO 581.5
LENGTH: 2076
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                               Matches 85;
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Best Local Similarity
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                          1249
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                                                                                                                                                                                                                                                                                1132 TAKKQEINQNTNATTEEKQVALNQVDQELATAINNINQADTNAEVDQAQQLGTKAINAIQ 1191
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                                                                                                                                                                  1192 PNIVKKPAALAQINQHYNAKLAEINATPDATNDEKNAAINTL-NQDRQQAIESIKQAN-- 1248
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  177 AVKELTS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/269,308
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                                                                                                        FTNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSKAAQDTLKNAVKELTS 368
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                                                          -TNAEVDQAATVAENNI--DAVQVDVVKKQAARDKITAEVAKRIEAVKQTPNATDEEKQA 1305
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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--PIVHGNNSRKDGNASTN--
                                                                                                                                                                                                                                                                                                                                                                                            9.5%; Score 171.5; DB 6; 20.0%; Pred. No. 0.0023; ative 78; Mismatches 174;
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-SADESVKGPNLTEISKKITES 221
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----SELETVKNSGLSTTSELA
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PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5815
LENGTH: 2076
                                                                                                                                                                                                                                                                                                                                   Query Match 9.5
Best Local Similarity 20.0
Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Staphylococcus aureus
10-072-851-5815
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  1306 AVNQINQLKDQAINQINQNQTNDQVDTTTNQAVNAIDNVEAEVVIKPKAIADIEKAVKEK 1365
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                                                                                   1249 -TNAEVDQAATVAENNI--DAVQVDVVKKQAARDKITAEVAKRIEAVKQTPNATDEEKQA 1305
                                                                                                                                                                   1192 PNIVKKPAALAQINQHYNAKLAEINATPDATNDEKNAAINTL-NQDRQQAIESIKQAN-- 1248
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                                         177 AVKELTS------PIVHGNNSRKDGNASTN-----SADESVKGPNLTEISKKITES 221
                                                                                                             117 FTNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKN 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 LSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCS-----TEFTNKLKSEHAVLG 314
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                                                                                                                                                                                                                                                                                         20 SVKGPNLTEISKKITESNAVVL--AVKEVETLLASIDELATKA---IGKKIGNNGLEA-- 72
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                                                                                                                                                                                                         ------NQSKNTSLL---SGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTE 116
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Zyskind, Judith W.
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Zamudio, Carlos
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Pred. No. 0.0023;
78; Mismatches 174;
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1540 QLAN 1543
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                                      ELTS
                                                                                                            LDNLTDDNAQRAI------LKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 364
                                                                                                                                                    IQPETKVKPAAREKIN-QKANELRAKINQDKEATAEERQVALDKINEFVNQAMTDITNNR 1479
                                                                                                                                                                                      LSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCS-----TEFTNKLKSEHAVLG 314
                                                                                                                                                                                                                              QQQIDNSLDSTDNEKEVASQALAKEKEKALAAIDQAQTNSQVNQAATNGVSA----IKI 1420
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R;Stevenson, B.; Bockenstedt, L.K.; Barthold, S.W.
Infect. Immun. 62, 3568-3571, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 19-209 < LIV>
A;Cross-references: EMBL:L42894; NID:g858722; PIDN:AAB37002.1; PID:g1695219
A;Experimental source: strain 28691
C;Genetics:
A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein C
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       RESULT
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S70277

I40281

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Pred. No. 2.2e
2; Mismatches
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Result

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Length 209

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A;Residues: 1-211 <RES>
A;Cross-references: EMBL:U04282; NID:g2314881; PIDN:AAC45540.1; PID:g434666
                                                                                                                                                                                                                                                                                                                                              PERS Microbiol. Lett. 124, 367-372, 1994
A;Title: Expression and sequence of outer surface protein C
A;Reference number: I40143; MUID:95154673
A;Accession: I40145
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Outer surface protein C - Lyme disease spirochete
C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Date: 12-reb-1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000
C; Accession: S70287
R; Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A; Title: Evidence for lateral transfer and recombination in OspC variation
A; Reference number: S70285; MUID:96296448
A; Accession: S70287
                                                                                                                                                                                                                              A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                          outer surface protein C precursor - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
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Best Local Similarity
Matches 136; Conserv
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A; Residues: 1-193 <LIV>
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                      77 AIGKKIHONNGLDTENNHNGSLLAGAYAISTLITOKLGGLKNEELKEKIAAVKKCSEEFT
                                       60 AIGKKI-GNNGLEANOSKNTSLLSGAVAISDLIAEKLNVLKNEELKEKIDTAKOCSTEET 118
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74.7%;
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                                                                                                                                                       Score 646; DB 2;
Pred. No. 1.2e-23;
8; Mismatches 32
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Pred. No. 2.3e-24;
0; Mismatches 25
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                                                                                                                                                                                  Length 211;
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A;Gene: ospC
C;Superfamily:
                                             A;Cross-references: EMBL:U08284; NID:g469561; PIDN:AAA21460.1;
                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-191 <RES>
                                                                                                                   A;Title: Humoral immune response to outer A;Reference number: I40153; MUID:94314437 A;Accession: I40153
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A; Residues: 1-193 <LIV>
A; Cross references: EMBL:L42898; NID:g858729;
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Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and record; Reference number: S70255; MUID:96296448
A;Accession: S70279
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                                           Genetics:
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Best Local S
Matches 135
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        Lyme
     disease spirochete
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Pred. No. 1.7e
16; Mismatches
surface protein
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L.7e-23;
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                                                PID: 9469562
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Similarity

35.6%; 73.9%;

Score Pred.

639; No. 2

DB 2; .3e-23;

Length

191;

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A;Cross-references: EMBL:X69596; NID:g311391; PIDN:CAA49306.1; R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. wol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in Osp A; Reference number: S70255; MUID:96296448
A;Accession: S70281
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684
R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschek, Med. Microbiol. Immunol. 182, 37-50, 1993
A-Title: Genetic heterogenity of the genes coding for the outer surface protein C pference number: S37726; MUID:93268136
Cccession: S37726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Fukunaga, M.; Hamase, A.
7. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence analysis A;Reference number: 140269; MUID:96025162
A;Accession: I40269
A;Status: preliminary; translated from GB/EMBL/DDBJ
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pecles: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence-rision 13-Feb-1998 #text_change 21-Jul-2000
C;Accession: G70218; I40269; S37726; S70281
C;Accession: G70218; I40269; S37726; S70281
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Yugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
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                                                                                                                          A; Experimental source: strain C; Genetics:
                                                                                                                                                               A;Molecule type: DNA
A;Residues: 19-210 <LIV>
A;Cross-references: EMBL:L42887; NID:g858715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-210 <KLE>
A;Residues: 1-210 <KLE>
A;Cross-references: GB:AE000792; NID:g3253098; PIDN:AAC66329.1; PID:g2689901;
A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia
A;Reference number: A70100; MUID:98065943
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                                                                                   A; Gene: ospC
C; Superfamily:
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A; Residues: 1-210 <JAU>
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A; Residues: 1-210 < RES>
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A; Residues: 1-210 <K
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A;Status: nucleic acid sequence not shown;
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                                                                                   Lyme disease spirochete surface
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Score 623.5; DB 2; Pred. No. 1.3e-22;
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                     210;
                                                                                                                                                                 PID:g1695212
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outer surface protein C precursor - Lyme disease spirochete (strain C;Species: Borrelia burgdorferi (Lyme disease spirochete)
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A;Molecule type: DNA
A;Residues: 1-50, 'E', 52-61, 'I', 63-117, 'D', 119-122, 'V', 124-173, 'D', 175-176, 'D', 178-209
A;Cross-references: EMBL:X83555; NID:g872019; PIDN:CAA58545.1; PID:g872020
C;Superfamily: Lyme disease spirochete surface protein C
E;1-18/Domain: signal sequence #status predicted <SIG>
E;19-209/Product: outer surface protein C #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Jauris-Heipke, S.; Liegl, G.; Preac-Mursic, V.; Roessler, J. Clin. Microbiol. 33, 1860-1866, 1995
A;Title: Molecular analysis of genes encoding outer surface A;Reference number: I40047; MUID:95395018
A;Accession: S69917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S69917; S72679
R; Jauris-Heipke, S.; Liegl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Borrelia burgdorferi (Lyme disease spirochete)
A;Variety: strain B. pacificus
C;Date: 06-Dec-1996 *sequence_revision 14-Feb-1997 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, January A; Reference number: S72679
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A; Residues: 1-209 < JAU>
A; Cross-references: EMBI
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                                                                                                       LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE 180
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                                                                                LKNGNAQLGLAAATDDNAKAAILKTNGTNDKGAKELKELSESVESLVKAAQVMLTNSVKE
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                                                                                                                                                                     IGQKIDANGLGVQANQNGSLLAGAYAISTLITQKLSALNSEELKEKIAKVKKCSEDFTNK
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                                                                                                     A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
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A;Experimental source: strain 26815
                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-193 <LIV>
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A:Accession: $72669
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C;Superfamily: Lyme disease spirochete surface protein
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A; Residues: 1-210 <JAU>
A; Cross-references: EMBL: X69589
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Best Local
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                                                               Local
3 CNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKAIG
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Pred. No. 2.1e-22;
                                             Score 619; DB 2
Pred. No. 2e-22;
2; Mismatches
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                                                                      DB 2;
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outer surface protein C precursor - Borrelia afzelii (strain PLj7)
C:Species: Borrelia afzelii
A;Variety: strain PLj7
C:Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000
C:Accession: S69922; S72675
R:Jauris-Heipke, S:; Liegl, G.; Preac-Mursic, V.; Roessler, D.; Schwab, E.; S
J. Clin. Microbiol. 33, 1860-1866, 1995
A;Title: Molecular analysis of genes encoding outer surface protein C (OspC)
A;Reference number: I40047; MUID:95395018
A;Accession: S69922
A; Molecule type: DNA
A; Residues: 1-212 < JAU>
                                                                              A; Status: nucleic acid sequence not shown
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A;Title: Evidence for lateral transfer and recombination A;Reference number: S70255; MUID:96296448
A;Accession: S70284
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A; Residues: 1-191 <LIV>
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Best Local Similarity
Matches 128; Conserv
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ce: strain 27579
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outer surface protein C - Lyme disease spirochete C; Species: Borrelia burgdorferi (Lyme disease spirochete) C; Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_C; Accession: S70268
R; Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A; Title: Evidence for lateral transfer and recombination:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Experimental source: strain PLj7 R;Roessler, D. submitted to the EMBL Data Library, A:Reference number: S72674 R;Accession: S72675
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C;Superfamily: Lyme disease spirochete surface protein
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A;Residues: 1-125,'V',127-154,'E',156-212 <ROB
A;Cross-references: EMBL:X81523; NID:g804956;
C;Genetics:
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A; Residues: 1-194 <LIV>
A; Cross-references: EMBL: L42888;
A; Cross-references: EMBL: L42888;
netLcs:
netLcs:
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A; Accession: $70268
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Local Similarity . 69.3%;
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                                                                                                                                       TNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
             ELTSPIV 186
                                    KLKGGHAELGLAAATDENAKKAILKTNGTKDKGAEELEKLFKSVESLAKAAKESLINSVK
                                                KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
                                                                                        GKKIQNNGLTAEQNQNGSLLAGAYAISALITKKLDELTKNSGELKGEVEKAKKCSEEFTN 120
                                                                                                     GKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVL-KNE-ELKEKIDTAKQCSTEFTN 119
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                                                                                                                                                                                                                                                            disease spirochete surface
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956; PIDN:CAA57243.1; PID:g804957
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R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.;
J. Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrelia burgdorferi outer surf. A;Reference number: I40104; MUID:95286481
A;Accession: I40104
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <RES>
A;Cross-references: EMBL:X84785: NTT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, J. Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrelia burgdorferi outer shareference number: 140104; MUID:95286481
A;Accession: 140125
A;Accession: 140125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outer surface protein C - Lyme disease spirochete (strain MUL) (fragment) C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-20 C;Accession: I40125; S54195
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C;Superfamily:
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C;Superfamily: Lyme
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A; Residues: 1-178 < RES>
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GIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLPKAAKEMLANSVKELTSPIV
                                      GLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKELTSPIV 186
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                                                                                                      LEANQSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTEFTNKLKSEHAVL 128
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Pred. No. 7.9e-22;
9; Mismatches 27;
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C;Accession: I40144; S70282

R;Stevenson, B.; Barthold, S.W.
FEMS Microbiol. Lett. 124, 367-372, 1994

A;Title: Expression and sequence of outer surface protein C
A;Reference number: I40143; MUID:95154673
A;Accession: I40144
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-210 <- RESSIONAL ASSIONAL ASSIONA
Search completed: March 18, 2002, 09:56:48 Job time: 371 sec
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A;Gene: OspC
C;Superfamily: Lyme disease spirochete surface protein C
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PVey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
Microbiol. 18, 257-269, 1995
A;Ftle: Evidence for lateral transfer and recombination in OspC variation in Lyme disea A;Reference number: S70255; MUID:96296448
A;Reference number: S70255; MUID:96296448
A;Status: nucleic acid sequence not shown
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
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A;Residues: 19-210 <LIV>
A;Cross-references: EMBL:L42893; NID:g858721; PIDN:AAB37001.1; PID:g1695218
A;Experimental source: strain 297
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G.G., Clayton R.A., R., Hickey E.K., Gwinn M., Richardson D., Salzberg S., Hanson M., I n Weidman I	f Borrelia	, Ryan R.W.; (OspC) from a North	, Soutschek E., C, an immunodominant ri.";	sic V., Schwab E., che outer surface burgdorferi.";	111a.		Q09857 schizosacch P08089 streptococc P05659 acanthamoeb P21875 borrelia he P55980 helicobacte O9utk5 schizosacch Q13439 homo saplen P02978 escherichia P51834 bacillus su P19401 streptococc Q39618 chlamydomon P08569 plasmodium

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OUTER SURFACE PROTEIN C
        MEDLINE-92219995; PubMed=1560779; Fuchs R., Jauris S., Lottspeich F
                                                                                                      Borrelia burgdorferi (Lymo Bacteria; Spirochaetales;
                                                                                                                                             OSPC
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Smith H.O., Venter J.
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J. Clin. Microbiol. 31:2570-2576(1993).
-!- FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE
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RESOLUTION OF THE SOLUTION OF 
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Best Local S
Matches 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPID
SEQUENCE
SEQUENCE FROM N.A.
STRAIN-SSP. HS1 SEROTYPE 3;
MEDLINE-93133110; PubMed-1484486;
Restrepo B.I., Kitten T., Carter
"Subtelomeric expression regions
                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
VARIABLE MAJOR OUTER MEMBRANE LIPOPROTEIN 3 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are highly polymorphic.";
MO1. Microbiol. 6:3299-3311(1992).
-i- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE
-FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
                                                                                                                                                                                                                                                  Q02448;
01-JUL-1993
                                                                                                                                                                                                                                                                                                            BORHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Restrepo B.I., Kitten T., Carter C.J., Infante D., Barbour A.G.; "Subtelomeric expression regions of Borrelia hermsii linear plasmids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SSP. HS1 SEROTYPE 24;
MEDLINE-93133110; PubMed-1484486;
                                                                                                                               Bacteria;
                                                                                                                                                Plasmid
                                                                                                                                                               Borrella hermsii.
                                                                                                                                                                                   VMP3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MACNNSGKDGNASANSADESVKGP----NLTEISKKITESNAVVLAVKEVETLLASIDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSCNNGGPE-----LKSDEVAKSDGTVLDLAKVSKKIKEASAFAASVKEVETLVKSVDEL
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214 /
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                                                                                                                            Spirochaetaceae;
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Pred.
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N-ACYL DIGLYCERIDE
; F1583F510246F7C7
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                                                                                                                                                                                                                                                                                         PRT;
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 C.J., Infante D., Barbour A. of Borrelia hermsii linear p
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                                                                                                                            Borrelia
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CRC64;
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Best Local :
 protein
J. Cell
[2]
                                                                        Nakajima H.,
Yamasaki M.;
                                                                                                                            SEQUENCE FROM N.A. STRAIN=X2180-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                            _YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
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P25386;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO
USO1 OR INT1 OR YDL058W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L04789; AAA22967.1; ... InterPro; IPR001800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1. ProDom; PD001149; Lipoprotein_6; 1. PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mol. Microbiol. 6:3299-3311(1992).

-i- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                        MEDLINE-91185402; Pu
Nakajima H., Hirata
                                                                                                                                                                                   Saccharomycetales;
NCBI_TaxID=4932;
[1]
                                         "A cytoskeleton-related gene, uso1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collal ween the Swiss Institute of Bioinformatics and the EMBL outs' European Bioinformatics Institute. There are no restrictions
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SUBCELLULAR LOCATION:
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transport in Saccharomyc Biol. 113:245-260(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                      PubMed=2010462;
ta A., Ogawa Y.,
                       in Saccharomyces
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39.8%;
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VARIABLE MAJOR OUTER MEMBRANE
LIPOPROTEIN 3.

N-ACYL DIGLYCERIDE (PROBABLE)
; 684C74D35F87C771 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 311.5; DB
Pred. No. 4e-08;
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                                                                                                                                                                                                                                                                                                                   PROTEIN USO1
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                                                                                        Yonehara
                         cerevisiae
                                            is required
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                                                                                        Τ.,
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JL; L03188; AAB00143.1; -.

JL; U53668; AAB66559.1; -.

R; A38455; A38455.

R; P80220; 1DIP.

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DISPENSABLE FOR THE PROTEIN FOR ASP/GLU-RICH (ACIDIC).

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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                              Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso Rifken L., Riles L., Taich A., Trevaskis E., Vignati D., Wilcon R., Waterston R., Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: ESSENTIAL COMPONENT OF THE NUCLEOSKELETON. POJROLECT IN CROSSLIKKING FILAMENTS OR ANCHORING OTHER MOLECU
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Saccharomycetales;
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UG-2001 (Rel. 40, Last annotation update)
PROTEIN (SPINDLE POLY BODY SPACER PROTEIN
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                                                                                    requires a license agreement (See http://www.an email to license@isb-sib.ch).
CAA77668.1; -. CAA51733.1; -. AAB64791.1; -.
                                                                                                                                                                                                                                                                                   BE REGULATED
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PIR: S34288; S34288.
SGD; S0002764; NUF1.
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                                                                Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G. Tummino P.J., Caruso A., Uria Nickelsen M., Mills D.M., II. Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E.,
                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-99120557; PubMed-9923682;
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      gastric
                             "Genomic
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Similarity 23.4%;
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NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL NUCLEAR FOR TYR-RICH.

ARG/TYR-RICH.

MW; 04FAA074BBBAA0BC8 CRC64;
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Q1-JUN-1994
Q1-JUN-1994
Q1-AUG-2001
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DOMAIN
  MEDLINE-90349606; PubMed=2117279;
Ketchum A.S., Stewart C.T., Stewart M., "Complete sequence of the Drosophila no transcript: conserved sequences in the
                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Pnhvdroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                     SEQUENCE FROM
TISSUE=Embryo;
                                                                                                                                          Drosophila melanogaster
                                                                                                                                                                   NISOYM
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FUNCTION: MAY BE NECESSARY FOR OR FUNCTION OF THE CYTOTOXIN.
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                                                                                                                                                                            (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last annotation updat
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                                                                                                                                                                   CHAIN, NON-MUSCLE (ZIPPER PROTEIN)
                                                                N.A.
                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                           (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
Stewart M., Klemarce myosin rosophila nonmuscle myosin tail and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agreement (See http://www.isb-sib
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Pred. No. 0.95;
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POLY-ASN.
POLY-B5E86B81CEBD0F2
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                                                                                                                             Tracheata; Hexapoda;
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d differential
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Best Local S
Matches 96
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Pfam: PF00063; myosin_head; 1.
Pfam: PF01576; myosin_tail; 1.
PfANTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSG; 1.
                  1315
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0005634; zip.
InterPro; IPR000048; IQ.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; Myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A36014; A36014.
PIR; B36014; B36014.
HSSP; P08799; IMND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myosin; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M35012; AAA28713.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splicing in the 5' untranslated sequence."; Proc. Natl. Acad. Sci. U.S.A. 87:6316-6320(1990)
                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                       26
                                                                                                                                                                                                                                                                                            Local Similarity
45
           IERARSELQEKCTK-LQQEAENITNQLEEAELKASAAVKSASNMESQLTEAQQLLE-EET
                                    VETILLASIDELATKAIGKKIGN--NGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEEL
                                                                                                                                                                                                                       VADLKEQLNERRVQVDEMQAQLAKREEELTQTLLRIDEESATKATAQKAQRELESQLAEI
                                                                                                                                                                                                                                                LTEISKKITESNAVV-----LAVKEVE----TLLASIDELATKAIGKKIG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: NONMUSCLE MYOSIN APPEARS TO BE RESPONSIBLE FOR CELLULARLIZATION. REQUIRED FOR MORPHOGENESIS AND CYTOKINESIS. ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY; CONTAINS 1 IQ DOMAIN.
                                                                                       TLKNAVKELTSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESNAVVLAVK--E
                                                                                                                TL-----KKSLEEETVNHEGVLADMRHKHSQELNSINDQLENLRKAKTVLEKAKG 1271
                                                                                                                                         VLGLDNLTDDNAQRAILKKHAN------KDKGAAELEKLFKAVENLSKA-----AQD 172
                                                                                                                                                                  QEDIEAEKAARAK----AEKVRRDLSEELEALKNELLDSLDTTAAQ--QELRSKREQELA 1221
                                                                                                                                                                                             NNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKLKSEHA 126
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1971
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                                                                                                                                                                                                                                                                               68;
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                                                                                                                                                                                                                                                                            Score 162.5; D
Pred. No. 1.9;
58; Mismatches
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25 KDA/50 KDA
50 KDA/20 KDA
                                                                                                                                                                                                                                                                                                                                                       ALPHA-HELICAL TAILPIECE (LMM).
GLOBULAR TAILPIECE.
MISSING (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                          ACTIN-BINDING.
REACTIVE SULFHYDRYL/ACTIN-BINDING
LIGHT MEROMYOSIN (LMM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQ.
COILED
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647 ISQITRESTEN--MSLLNKEIQDLYDSKSDISIK-LGKEKSSRILAEERFK---LLSNTL 700

LTEISKKITESNAVVLAVKEVETLLASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAY 85

Matches

96;

Conservative

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Mismatches

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Indels

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Gaps

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                                                                                                                                                                                                                                            EMBL; L01992; AAA34783.1; -
EMBL; X73541; CAA51948.1; -
EMBL; Z73542; CAA82174.1; -
PIR; S38173; S38173;
SGD; S0001803; MLP1.
                                                                                                 DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Remacha
                                                                                                                                                                                                      DOMAIN
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the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         new open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cerevisiae chromosome XI contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93247549; PubMed=8483450;
Koelling R., Nguyen T., Chen E.Y., Botstein D.;
"A new yeast gene with a myosin-like heptad repeat structure.";
Mol. Gen. Genet. 237:359-369(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q02455;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94205265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994
20-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :- SIMILARITY: SOME, TO THE TPR ONCOGENE.
:- CAUTION: REF.2 MISQUOTES THE GENE NAME AS "MPL1"
  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENCE FROM N.A. (Cantalejo J.G INE-94205265; PubMed-8154186; INE-94205265; PubMed-8154186; G., Esteban P.F., Baladron V., Gonzalez G.A., Cantalejo J.G Cha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J. Complete sequence of a 15,820 bp segment of Saccharomyces complete sequence of a 15,820 bp segment of MPL1 genes and the UBI2 and 
                                                                                                                   d coil; DNA repair.
N 69 487
N 531 1678
N 1834 1866
N 1834 1866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR YKR095W OR YKR415
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(Rel. 29,
(Rel. 40,
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8.9%;
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
R -> A (IN REF. 1).
RW; 683A0D34C9066867 CRC64;
Score 159.5;
Pred. No. 2.4
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                       DB 1;
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Revuelta J.L.;
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01-FEB-1994
30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                               Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Copell R., Copey T., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (see http://www.isb-or send an email to license@isb-sib.ch).
                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                               Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-94150718; PubMed-7906398;
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KDA PROTEIN T05G5.9 IN CH
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Best Local S
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Pfam; PP01465; GRIP; 1.
Pfam; PP01465; GRIP; 1.
Hypothetical protein; Coiled c
DOMAIN 75 137
DOMAIN 160 509
DOMAIN 562 641
SEQUENCE 705 AA; 80637 MW;
                                                                                                                                                                                                                                                                              01-APR-1993
01-APR-1993
01-OCT-1996
                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-92315338; PubMed-1617731;
Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
Galinski M.R., Medina protein complex of Plasmodium viv
                         between
the Euro
                                                                         "A reticulocyte-binding protein complex of Plasmodiun merozoites.",
Cell 69:1213-1226(1992).
-i- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECHUMAN RETICULOCYTE CELLS.
-i- SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE).
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                                   This SWISS-PROT entry is copyright. It is produced throughout the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                           Plasmodium vivax (str
Eukaryota; Alveolata;
NCBI_TaxID=31273;
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European Bioinformatics Institute
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AC P15215; 024373; 09Vyl8;

DT 01-APR-1990 (Rel. 14, Created).

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE LAMININ GAMMA-1 CHAIN PRECURSOR (LAMININ B2 CHAIN).

GN LAMB2 OR LAMG1 OR LAMG1 OR CG3322.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Pbhydroidea; Drosophilidae; Drosophila.
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 STRAIN-CANTON-S, AND OREGON-R; MEDLINE-9129161; PubMed-1840513; Chi H.-C., Juminaga D., Wang S.Y., "Structure of the Drosophila gene: DNA Cell Biol. 10:451-466(1991).
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RA Adams M.D. (Calniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D. (Calniker), Fubmed=10/31132;
RA Adams M.D. (Calniker), E.E., Holt R.A., Hoskins R.A., Galle R.F., RA Adams M.D. (Calniker), S.E., Holt R.A., Shang Q., Chen L.X., Rafacon S.N., Evandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Barlaw R.M., Bast R.A., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Aphayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Barlaw R.M., Bouck J., Brokatelin P., Brottler P., Ratellow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Barlaw R.M., Bouck J., Brokatelin P., Brottler P., Ratellow R.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Gland P., Leitz S.M., Ra Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyaum C., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Keatt C., Kravitz S., Kulp D., Lai Z., RA Harris N.L., Harvey D., Keatt C., Kravitz S., Kulp D., Lai Z., Lin X., Lii Z., Lin X., Lai Z., Lin X., Lai Z., Lin X., Lai Z., Lin X., Lai Z., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Ling Y., Lii X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., McShrefi A., Ra Merson D.R., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.L., Raft C., Krapheton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Shen H., Shen H., Shen H., Ra Shen T., Shen M., Shen H., Shang X., Wang S., Yao Q.A., And Lai R., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H.,
"CDNA and amino acid sequences of Drosophila laminin B2 chain.";
Nucleic Acids Res. 16:7205-7205(1988).

-I- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

-I- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOU TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END

-I- SUBCELLULAR LOCATION: BASEMENT MEMBRANES (MAJOR COMPONENT)

-I- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88303364; PubMed=3405777; Chi H.-C., Hui C.-F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=OREGON-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 344-1639 FROM N.A.
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"Drosophila laminin: sequence of B2 subunit and "brosophila lamining embryogenesis.";

three subunits during embryogenesis.";

J. Cell Biol. 109:2441-2453(1989).
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EMBL; M58417; AAA28664.1; -.
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EMBL; X07806; CAA3065.1; -.
PIR; A31483; MMFFB2.
HSSP; P02468; ITLE.
F1yBase; FBgn0002528; LanB2.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000186; LamMT.
InterPro; IPR000184; Laminin_B.
InterPro; IPR000034; Laminin_B.
InterPro; IPR000044; Laminin_EGF
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SMART; SM00136; LamNT; 1.

SMART; SM00136; LamNT; 1.

PROSITE; PS00022; EGF_1; 8.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01248; LAMNIN_TYPE_EGF; 11.

PROSITE; PS01248; LAMNIN_TYPE_EGF; 11.

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ProDom; PD003031; Laminin_B; 1.
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SMART; SM0001; EGF_like; 1.
SMART; SM00281; LamB; 1.
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DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
SIMILARITY: CONTAINS 1 LAMININ -TERMINAL DOMAIN
SIMILARITY: CONTAINS 11 LAMININ EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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                                                                                                                   isolation of a collection of D. melanogaster cDNAs homologous to sequences in the Human Gene Index database.";
MO1. Gen. Genet. 261:64-70(1999).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
-!- CAUTION: REF:2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS IN POSITIONS 920 AND 930.
                                                                                                                                                                                                                                                                                                                                                                                   Caggese C., Ragone G., Perrini B. Caizzi R., Barsanti P., "Identification of nuclear genes
                                                         between
                                                                                             This
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30-MAY-2000 (Re:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 626-944 FROM N.A.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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20-AUG-2001 (Rel. 40, Last ann
CALCIUM-BINDING MITOCHONDRIAL
ANON-60DA OR CG4589
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SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0019886;
                                                                                                                                                                                                                                                                                                                                                                                                                        703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 ISKKITESNAVVLAVKEVETLLASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAIS
                                                                                                                                                                                                                LGLDNLTDDNAQRA-----ILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n; PF00428; 60s_ribosomal; 1.
pF01334; Bacteriofer; 1.
pF02731; DUF223; 1.
pF02736; efhand; 2.
pF00036; efhand; 2.
pF00185; HR1; 1.
pF00056; idh; 1.
pF00056; idh; 1.
                                                                                                                                                                               KDLSKLVNDIHDSAKEIQDIANEMRDKEETVPDKAKELKA-EPAFKDTAKTLKDNAKDL
                                                                                                                                                                                                                                                           LSDK-----AIEELISLLDKEQVLQAE---QKIEKAIAKSMKEAEKLKSEVDKAD
                                                                                                                                                                                                                                                                                    ANQSKNTSLLSGAYAISDLIA--EKLNYLKNEELKEKIDTAKQCSTEFTNKLKSE--HAV 312
                                                                                                                                                                                                                                                                                                                                        VLKETSDEA-RLKHIEAVLEKFDADKDGVVTVNDIRKVLES-----IGRDNIK
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                                                                  P78969;
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drion; Calc
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; IPR002024;
; IPR003871;
; IPR002048;
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711 EF-HAND 1
Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
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E -> Q (
K -> G (
Q -> B (
K -> B (
C -
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Pred. No. 1.7;
52; Mismatches
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2 (IN REF. 2).
3 (IN REF. 2).
4 (IN REF. 2).
5 (IN REF. 2).
6 (IN REF. 2).
5 (IN REF. 2).
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood V., Rajandream M.A., Barrell B.G., Rieger M.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: REDUIRED FOR CELL DIVISION. IT IS A COMPONENT OF
CDC12 'SPOT', A STRUCTURE THOUGHT TO MARK THE SITE OF SEPTA
                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00063; myosin_head; 1. PRINTS; PR00193; MYOSINHEAVY. PR0000; PD0000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAY WORK IN CONJUNCTION WITH MYO3.
-I- SUBUNIT: BINDS TO CDC4 AND RLC1.
-I- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD
-I- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe.
Cell Motil. Cytoskeleton :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYO2
                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                  NP_BIND
                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                          Alkylation
                                                                                                                                                                                                                                                                                                                                                       Myosin; Actin-binding; ATP-binding; Coiled coil; Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       May K.M., Watts F.Z., Jones N., Hyams J.S.;
"Type II myosin involved in cytokinesis in the fission yeast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896
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                                                                                                                                                                                                                                          MOD_RES
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 112
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                                                                                    842
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                             QNENLQRESASLKQINNELESELLEKTS-----KVETLLSEQ-----NELKEKLSLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR SPCC645.
QCSTEFTNKLKS--EHAVLGLDNLTDDNAQ-RAILKKHANKDKGAAELEKLFKAVENLSK
                                                                                  KQQNSKSEVERDLVETNNSLTAVENLLTTERAIALDKEEILRRTQERLANIEDSFSETKQ
                                                                                                              KDGNASANSADESVKGPN-LTEISKKITESNAVVLAVKEV----ETLLASIDE-----
                                                     ----LATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAK
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                                                                                                                                            88;
                                                                                                                                                      Similarity
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                                                                                                                                         Score 154; DB Pred. No. 3.3; 76; Mismatches
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                                                                                                                                                                                                                                                    ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                             ALKYLATION (BY SIMILARITY).
S -> R (IN REF. 1).
                                                                                                                                                                                                                                                                                               COILED COIL (POTENTIAL).
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                                                                                                                                                                                                              D71D51D6578192BA CRC64
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                                                                                                                                                      DB 1;
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15-DEC-1998
15-DEC-1998
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                                                                                                                                                                                                                                                                     ECOLI
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                       PRINTS; PR00280; CHANLCOLICIN.

PRODOM; PD002657; Channel_colicin; 1.

PROSITE; PS00276; CHANNEL_COLICIN; 1.

Antibiotic; Bacteriocin; Plasmid; Transmembrane.

TRANSMEM 505 525 POTENTIAL.
                                                                                     EMBL; x87834; CAA61099.1; -.
EMBL; U27452; AAB41288.1; -.
InterPro; IPR000293; Channel_colicin.
Pfam; PF01024; Colicin; 1.
                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Pilsl H., Braun V
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Plasmid ColK-K235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              "Strong function-related homology between the pore-forming colicins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=562;
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                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE CHANNEL FORMING COLICIN FAMILY.
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121 LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE 180

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   MEDLINE=96296448; PubMed=8709845;
Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last amnotation updat
0UTER SURFACE PROTEIN C (FRAGMENT).
Borrella burgdorferi (Lyme disease spirochete).
                                SEQUENCE FROM N.A. STRAIN-28691;
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                                                       Bacteria; Spirochaetales;
NCBI_TaxID=139;
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EMBL; U04240; AAC45538.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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Wang I.-N., Dykhuizen D.E., Submitted (OCT-1997) to the EMBL; AF029866; AAB86549.1;
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Pfam; PF01441; Lipoprotein_6; 1.
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NCBI_TaxID=139;
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Pfam; PF01441; Lipoprotein_6; 1.
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Mol. Microbiol. 18:257-269(1995).
EMBL; L42894; AAB37002.1; -
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                                                                                                                                                               Score 889; DE Pred. No. 1.362; Mismatches
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EMBL/GenBank/DDBJ
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Wang I.-N. Dykhuizen D.E., Dunn J.J.,
Submitted (OCT-1997) to the EMBL/GenB.
Submitted (OCT-1997) to the EMBL/GenB.
EMBL; AF029871; AAB86554.1; -.
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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NCBI_TaxID=139;
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22; Mismatches
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                                                                                                                                         MEDLINE-94041630; PubMed-8225587;
Padula S.J., Sampieri A., Dias F., Szczepansk
Nolecular characterization and expression of
American strain of Borrelia burgdorferi.";
Infect. Immun. 61:5097-5105(1993).
EMBL; U01892; AAA16057.1; -.
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
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Matches 133
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01-JUL-1997 (T)
01-JUL-1997 (T)
01-JUN-2001 (T)
0UTER SURFACE (
                                                 Stevenson B., Barthold S.W.;
"Expression and sequence of outer surface American isolates of Borrelia burgdorferi.
FEMS Microbiol. Lett. 124:367-372(1994).
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=25015;
MEDLINE=95154673; PubMed=7851744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q44720
Q44720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi
Bacteria; Spirochaeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia tanukii.
Bacteria; Spirochaetales;
NCBI_TaxID=56146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-FI81T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTEFT 118
                      004282;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spirochaetales;
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202 /
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(TIEMBLrel. 04, Last sequence up
(TIEMBLrel. 17, Last annotation
E PROTEIN C (FRAGMENT).
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                      AAC45540.1;
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21536 MW;
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70.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             spirochaetaceae; Bor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukui T., Yanagihara Y.; ospC, partial cds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spirochaetaceae; Borrelia
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Last sequence update)
Last annotation updat
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Pred. No. 2.2e
22; Mismatches
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1.2e-23;
les 31;
                                                                                                       protein .";
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Matches 135; Conser
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Best Local
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Plasmid.
NON_TER
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
OUTER SURFACE PROTEIN C PRECURSOR (FRAGMENT).
OSPC.
                                                                                                                                                                                                                                                                                                                                                                                                                            Q9RQR8;
Q9RQR8;
01-MAY-2000
                                                                                                                                                                                                                              Hofmeister E.K., Glass G.E., Childs "Population dynamics of a naturally Borrelia burgdorferi clones.", Infect. Immun. 67:5709-5716(1999). EMBL; AF074465; AAD23912.1; InterPro; IPR001800; Lipoprotein_6.
                                                                                                                                                                                SEQUENCE
 137
                      119
                                                                                                                                                                                                                           Pfam; PF01441;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A STRAIN=3B6';
                                                                                                                                                                                                                                                                                                                                                             Plasmid cp26.
                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi (Lyme disease spirochete).
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
SEQUENCE 211 AA; 22603 MW; 63984BA6D8743ED5
                                                                                                                                                                                                                                                                                                  MEDLINE=20002545;
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=139;
                                                              61
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          NKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAV
                                     MACNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKA
KKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSV
                                                                                 ISCNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MACNNSGKDGN-ASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKLKSSHTELGKQDAQDDDAKKAILRTHNTKDKGAEELDKLFKAVENLSKAAKEMLSNSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISCNNSGKDGNAASTNPADESVKGPNLTEISKKITDSNAVVLAVKEVGALLTSIDELATK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KELTSPVV
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                                                                                                                                                                                                              PD001149;
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201 AA;
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186
                                                                                                                                                                                                                         Lipoprotein_6;
                                                                                                                                                                                                                                                                                      PubMed=10531219;
Glass G.E., Childs
                                                                                                                                                                                                              Lipoprotein_6;
                                                                                                                                                                               201
21457 MW;
                                                                                                                        35.8%; Score 644; DE 73.4%; Pred. No. 2.76 tive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.9%;
72.3%;
                                                                                                                                                                                                                                                                                                                                                   Spirochaetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 646;
Pred. No. 2.
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                                                                                                                                                                             806F198295101B07 CRC64;
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                                                                                                                                   5644;
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                                                                                                                                                                                                                                                                          occurring
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                                                                                                                                     DB 2;
1.7e-23;
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.3e-23;
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01-NOV-1996 (TrEMBLrel. 101, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
0UTER SURFACE PROTEIN C (FRAGMENT).
BOTTELIA burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID-139;
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01-MAY-1997 (TREMBLrel. 03, Last sequence up
01-UN-2001 (TrEMBLrel. 17, Last annotation
0UTER SURFACE PROTEIN C (FRAGMENT).
MEDLINE=94314437; PubMed=8039891;
Fung B.P., McHugh G.L., Leong J.M., Steere A.C.;
"Humoral immune response to outer surface protein C of E
burgdorferi in Lyme disease: role of the immunoglobulin
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID=139;
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EMBL; L42898; AAB37007.1; -.
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MEDLINE-97478003; PubMed-9336916;
Ras N.M., Postic D., Foretz M., Baranton
"Borrelia burgdorferi sensu stricto, a be
U.S.A.'?";
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-TUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
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ProDom; PD001149; Lipoprotein_6; 1.
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Infect. Immun. 62:3213-3221(1994).
EMBL; U08284; AAA21460.1;
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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Pred. No. 4.4e-23;
0; Mismatches 26;
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                                        01-JAN-1998 (TremBLrel. 05, Created)
01-JAN-1998 (TremBLrel. 05, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT).
Bacteria;
    Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borr
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0UTER SURFACE PROTEIN C (FRAGMENT).
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Borrella burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrel.
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InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
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ALIGNMENTS

Chimeric - Chimeric -Borrelia sp chimeric ospC protein SEQ ID NO: 03-APR-2001 (first entry) AAB62719; AAB62719 standard; Protein; 28-DEC-2000. WO200078966-A1. Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick. Borrelia sp. Borrelia sp. 367 Å 42

(UYNY) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC. 18-JUN-1999; 99US-0140042

19-JUN-2000; 2000WO-US16915

Dattwyler RJ, Seinost G, Dykhuizen D, Luft BJ, Gomes-Solecki

WPI; 2001-050113/06. N-PSDB; AAF29023.

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                                                 9908-0140042
                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                 entry)
                                                                                                                                           disease; vaccine; chimeric protein; tick.
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                                                                                                                                                                protein SEQ ID NO:
      Dykhuizen
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    D,
    Luft BJ,
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  Gomes-Solecki
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              19-JUN-2000; 2000WO-US16915
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Chimeric - Borrelia
                                                                                                    Borrelia sp chimeric ospC protein SEQ ID NO:
                                                 WO200078966-A1
                                                                                     Borrelia; ospC; Lyme disease; vaccine;
                                                                                                                        03-APR-2001
                                                                                                                                                     AAB62718 standard; Protein;
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Lyme disease are used
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99.7%;
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Pred. No. 2e-108;
1; Mismatches
                                                                                    chimeric protein; tick.
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87.5%; Pred. No. 2.1e-93;
Live 20; Mismatches 25; 1
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87.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              BIOTECHNOLOGIES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lyme
         Protein;
                                                                                                                                                                                                                                                            85.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease;
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                                                                                                                                                                                                                                                                                                                                                 English
         391
                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                Dykhuizen
                                                                                                                                                                                                                                                           Score 1538;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; chimeric protein; tick.
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     FOUND
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                                                                                                                                                                                                                                                            .8e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                Luft
                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                ВJ,
                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Gomes-Solecki
                                                                                                                                                                                                                                                                                                                          These may
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                                                                                                                                                                                                                                                                                                                                 proteins
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Matches
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                                                                                                                                                                                                                                                                                                    Claim 43;
383
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The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compositions of OspC polypeptides Lyme disease are used to immunize to Lyme disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dattwyler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric -
Chimeric -
362 ANSVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
mes 317; Conserv
                                                                                                                                                                                                                                                                EDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEML
                                                                                  ATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCS
                                                                                                                                                           TSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDEL
                                                                                                                                                                                                     ACNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETILLASIDELATKAI
                          teftnklksehavlgldnltddnaqrailkkhankdkgaaeleklfkavenlskaaqdtl
                                                                                                                                              tspivhgnnsrkdgnastnsadesvkgpnlteiskkitesnavvlavkevetllasidel
                                                                                                                                                                                                                                                                                                                           scnnsgkdgnasansadesvkgpnlteiskkitesnavvlavkevetllasidelatkai
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DB; AAF29040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 144-145; 160pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ospC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia
Borrelia
 368
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0140042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyme disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp.
                                                                                                                                                                                                                                                                                                                                                                                   85.1%; Score 1530; DB 22;
86.4%; Pred. No. 1.4e-91;
Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dykhuizen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from strains animals and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s of Borrelia
detect immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gomes-Solecki
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                                                                                                                                                                                                                                                                                                                                                                                                                  391;
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est Local Similarity
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                                                                                                                                                                                                                                                                  The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea
                                                                                                                                                                                                                                                                                                             Claim 43; Page 86-87; 160pp;
                                                                                                                                                                                                                                                                                                                                      Compositions of OspC p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-2001
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                                                                                                                                                                                                                                                                                                                               to Lyme
                                                                                                                                                                                                                                                                                                                                                                                          Dattwyler RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200078966-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia sp chimeric ospC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB62713;
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                                                                                                                                                                                                                                                                                                                                                                                                         (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                            232
                                                              181
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                                                                                                               120
            292
                                                                                                                                61
                                                                                                                                               61
                                                                                                                                                              Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                           ELTSPIVHG-----NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEI
                                                                                             KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
                                                                                                                             ETLLASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLK
                                                                                                                                                                                                                                                                                                                                                                        2001-050113/06
           EKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVE
                          etllasidelatkaigkkiqqngglaveaghngtllagaytisklitqkldglknseklk
                                                                                                                                                                                                  311;
                                                                                                                                                                                                                                                                                                                                disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ospC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia
Borrelia
                                                                                                                                                                                                                                            377
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
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                                                                                                                                                                                                                                                                                                                                                                                         Seinost G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyme disease; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp.
                                                                                                                                                                                                         82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                       polypeptides from strains to immunize animals and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                         Dykhuizen D,
                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377
                                                                                                                                                                                                          Score 1485.5;
Pred. No. 9.86
                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chimeric
                                                                                                                                                                                                          5; DB 22; Length 377;
.8e-89;
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O:
                                                                                                                                                                                                                                                                                                                                                                                         Luft BJ,
                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30
                                                                                                                                                                                                                                                                                                                                      of Borrelia which cause detect immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; tick.
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                                                                                                                                                                                                                                                                                                                                                                                          Gomes-Solecki
                                                                                                                                                                                                  9;
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N-PSDB;
                                                                                                                                                                    The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzeli or B. garini. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
                                                                                                                                                                                                                     Compositions of OspC polypeptides Lyme disease are used to immunize to Lyme disease -
                                                                                                                                                                                                                                                                                                                                                             Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB62711 standard;
                                                                                                                                                Sequence
                                                                                                                                                             to Lyme disease.
                                                                                                                                                                                                      Claim 43; Page 81;
                                                                                                                                                                                                                                                                    Dattwyler RJ,
                                                                                                                                                                                                                                                                                 (UYNY ) UNIV N
(BROO-) BROOK
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                                                                                                                                                                                                                                                                                                                                                WO200078966-A1
                                                                                                                                                                                                                                                                                                                                                                                   Borrelia;
                                                                                                                                                                                                                                                                                                                                                                                               Borrelia sp chimeric ospC protein
                                                                                                                                                                                                                                                                                                      18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
                             121
                                          121
 181
              181
                                                                                                                    Local
                                                       61
                                                                     62
                                                                                                                                                                                                                    Lyme
                                                                                  8
                                                      2001-050113/06.
DB; AAF29015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311;
                                                                                                                    Similarity '
                                                                                                                                                                                                                                                                                         UNIV NEW YORK STATE RES
                                                                                                                                                                                                                    disease
                                                                                                                                                                                                                                                                                                                                                                                  ospC;
                                                                                                                                                 373 AA;
                                                                                                                                                                                                                                                                                                                                                              Borrelia
                                                                                                                                                                                                                                                                                                                                                                     Borrelia
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                  BIOTECHNOLOGIES
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                                                                                                                                                                                                                                                                                                       99US-0140042
                                                                                                                                                                                                                                                                                                                                                                                  Lyme
                                                                                                                                                                                                      160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                             sp.
                                                                                                                    82.5%;
                                                                                                                                                                                                                                                                                                                                                                                   disease;
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و
                                                                                                             22;
                                                                                                                                                                                                                                                                   Dykhuizen
                                                                                                                                                                                                                                                                                                                                                                                                                                          373
                                                                                                                   Score 1484;
Pred. No. 1.
                                                                                                                                                                                                                                                                                  ES FOUND
                                                                                                                                                                                                                                                                                                                                                                                  vaccine;
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                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                SEQ
                                                                                                                                                                                                                           from strains of Borrelia which cause animals and detect immune responses
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                                                                                                                                                                                                                                                                                                                                                                                                ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   chimeric
                                                                                                             DB 22;
1.2e-88;
nes 34;
                                                                                                                                                                                                                                                                    Luft
                                                                                                                                                                                                                                                                     BJ,
                                                                                                                                                                                                                                                                                                                                                                                  protein;
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AAB62729
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                                                                                              Matches
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Best Local :
                                                                                                                                                                                                                               Compositions of OspC polypeptides from strains Lyme disease are used to immunize animals and \dot{\rm c} to Lyme disease -
                                                                                                                                                                 The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
                                                                                                                                         Sequence
                                                                                                                                                            င
                                                                                                                                                                                                              Claim 43; Page 125-126; 160pp;
                                                                                                                                                                                                                                                                    N-PSDB; AAF29033.
                                                                                                                                                                                                                                                                                             Dattwyler RJ,
                                                                                                                                                                                                                                                                                                                                         18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric -
Chimeric -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB62729 standard;
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(BROO-)
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                                                                                                                                                                                                                                                                                                                                                                            28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia; ospC;
121
                                                                                                                                                                                                                                                                                                                                                                                             WO200078966-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia sp chimeric ospC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
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                        85
                                        62
                                                          25
                                                                                                      Local Similarity
                                                                           N
                                                                                                                                                         Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
     LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE 180
                     2001-050113/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAKEMLANSVKEL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aakemlansvkel 373
                                                                                              310;
                                                                                                                                                                                                                                                                                                              UNIV NEW YORK STATE RES
BROOK BIOTECHNOLOGIES IN
                                                                                                                                         397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia sp.
Borrelia sp.
                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry
                                                                                                                                                                                                                                                                                             Seinost G,
                                                                                                                                                                                                                                                                                                                                         99US-0140042
                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyme disease; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                    82.4%;
83.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                            Dykhuizen D,
                                                                                             Score 1481; DB Pred. No. 2e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397
                                                                                                                                                                                                                                                                                                               INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                         chimeric
                                                                                                                                                                                                                                                                                             Luft BJ,
                                                                                                             DB 22;
                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                         s of Borrelia which cause detect immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
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                                                                                                                                                                                                                                                                                             Gomes-Solecki M;
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Best Local Similarity
Matches 310; Conserv
                                                                       The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads to Lyme disease.
                                                                                                                                                             Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease -
                                                                                                                                                                                                    WPI; 2001-050113/06.
N-PSDB; AAF29020.
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(BROO-)
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Chimeric -
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BROOK BIOTECHNOLOGIES IN
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Borrelia
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Score 1480; D. Pred. No. 2.2e 25; Mismatches
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2.2e-88;
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                   The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
                                                       Claim
                                                                    Compositions of OspC polypeptides Lyme disease are used to immunize to Lyme disease -
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Sequence
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                                                                                                                    Dattwyler RJ,
                                                                                                                                 (UYNY ) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC.
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)B; AAF29043.
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                                                       43;
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Query

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The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelid or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads

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                                                                                                                                                                   Compositions of OspC |
Lyme disease are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric -
Chimeric -
                                                                                                       Claim 43; Page 131;
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N-PSDB; AAF29016.
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                                                                Dattwyler RJ,
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                                                                                                                                                                                                                                                                                                               emlansvkel
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Borrelia
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                                                               Seinost G,
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                                                                                                                                                                          gp.
                                                               Dykhuizen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
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Pred. No. 3
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             from strains animals and o
                                                               Luft BJ,
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           s of Borrelia which cause detect immune responses
                                                               Gomes-Solecki
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Best Local
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                   Dattwyler RJ,
                                      (UYNY ) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
                                                                          18-JUN-1999;
                                                                                              19-JUN-2000; 2000WO-US16915
                                                                                                                                         WO200078966-A1
                                                                                                                                                                                               Borrelia; ospC; Lyme disease;
                                                                                                                                                                                                                    Borrelia sp
                                                                                                                                                                                                                                            03-APR-2001
                                                                                                                                                                                                                                                                  AAB62710;
                                                                                                                                                                                                                                                                                     AAB62710 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides compositions comprising ospC proteins an chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelli or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads to Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 43; Page 83-84; 160pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETLLASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLK 291
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70.3%;
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                                                                                                                                                                                                                                                                                      374 AA
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                                                                                                                                                                                             vaccine; chimeric protein; tick.
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                  Luft
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                  BJ',
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                 Gomes-Solecki M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 43; Page 78-79; 160pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                                          Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                      AAB62728;
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                   19-JUN-2000;
      18-JUN-1999;
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                                                                              ospC;
                                                          Borrelia
Borrelia
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                                                                                                                                                                                                                                                                                                                                                              Conservative
                   2000WO-US16915
                                                                                                         (first entry)
      99US-0140042
                                                                             Lyme disease;
                                                                                                                                                                      372
                                                                                                                                    Protein;
                                                          gp.
                                                                                                                                                                                                                                                                                                                                                             69.4%; Score 1248.5; 71.0%; Pred. No. 2.10 Live 42; Mismatches
                                                                                           protein
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Lyme disease are used
to Lyme disease -
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                                                                                                                                                                                                    Local Similarity
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  AAKEMLANSVKEL
                              NAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAK
                                                        ASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIE
                                                                                          {\tt ltspvvaespamvnnsgkdgntsansadesvkgpnlteiskkitesnavvlavkevetll}
                                                                                                   LTSPIVHG-----NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLL
                    kakkcseeftaklkgehtdlgkegvtddnakkailktnndktkgadeleklfesvknlsk
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Pred. No. 3.66
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
/cgn2_6/ptodata/2/paa/US081_COMB.pep:*
/cgn2_6/ptodata/2/paa/US082_COMB.pep:*
/cgn2_6/ptodata/2/paa/US083_COMB.pep:*
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US-09-596-746A-40
US-09-596-746-40
US-09-596-746-72
US-09-596-746-73
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164.485 Million cell updates/sec
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96-746-7	-09-596-7	-09-596-746A-5	-09-596-746A-	-09-596-746-5	09-596-746A-	-09-596-746-6	-09-596-746-3	-09-596-746A-	-09-596-746A-6	-09-596-746-6	-09-596-746A-	-09-596-746-8	-09-596-746-3	-09-596-746A-	-09-596-746-6	-09-596-746-2	-09-596-746A-3	US-09-596-746A-28	-09-596-746-2	-09-596-746A-2	-09-596-746A-	-09-596-746-6	-09-596-746A-	9-596-746-8	-596-746-3	-09-596-746A-	-09-596-746-6	9-596-746-2	-09-596-746A-3	-09-596-746A-	-09-596-746-3	S-09-596-746A-2	S-09-596-746A-	-596-746-7	-596-746A-
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ALIGNMENTS

US-09-596-746A-42

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; FEATURE:
; OTHER INFORMATION: OSPC Chimera
US-09-596-746A-42
                                                                                                                                                                                                SOFTWARE: Fa
SEQ ID NO 42
LENGTH: 368
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 42, Application US/09596746A
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
Matches 368;
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/596,746A CURRENT FILING DATE: 2000-06-19 PRIOR APPLICATION NUMBER: US 60/140,042 PRIOR FILING DATE: 1999-66-18 NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Groups of Borrelia burgdorferi
TITLE OF INVENTION: Borrelia afzelii That Cause Ly
FILE REFERENCE: 2631.1002-001
                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                     FastSEQ for Windows Version 4.0
  Conservative
                  100.0%;
  0;
Score 1798; DB 19; Pred. No. 5.6e-124; Mismatches 0;
  Indels
                                     Length 368;
                                                                                                                                                                                                                                                                                                                                                                               Disease in Humans
  0
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APPLICANT: Seinost, Geraiu
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: OSPC Chimera
US-09-596-746-42
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Best Local Similarity
Matches 367; Conserv
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SEQ ID NO 42
LENGTH: 367
TYPE: PRT
ORGANISM: Artificial Sequence
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                   182
                                   61
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TSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDEL
                                                                                     GKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKL
                                                                                                  GKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKL 121
                                                                                                                                      SEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEM
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                        Score 1793; DB 19;
; Pred. No. 1.3e-123;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               Cause Lyme Disease in Humans
                                                                                                                                                                                                                 Length 367;
                                                                                                                                                                                         Indels
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             241
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Sequence 74, Application US/09596746
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Scinost, Gerald
APPLICANT: Scinost, Gerald
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdd
TITLE OF INVENTION: Borrelia afzelii That Cal
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 1290-06-18
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: Fas
SEQ ID NO 74
TRNGTH: 391
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Best Local Similarity
Matches 366; Conserva
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 ANSVKEL
                 ANSVKEL 368
                                                EDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEML
                                                                                                     ATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCS
                                                                                                                     ATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCS 301
                                                                                                                                                             TSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDEL
                                                                                                                                                                             TSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDEL
                                                                                                                                                                                                                   KSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKEL
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative
391
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                                                                                                                                                                                                                                                                                                                                                                                        Score 1790; DB 19;
Pred. No. 2.4e-123;
1; Mismatches 0;
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; Sequence 40, Application US/09596746A

; GENERAL INFORMATION:
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SEQ ID NO 74
LENGTH: 392
TYPE: PRT
ORGANISM: OSPC Chimera
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Best Local S
Matches 366
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykutizer, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
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99.7%; Pred. No. 2.46
tive 1; Mismatches
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2.4e-123;
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Sequence 40, Application US/09596746
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes Solecki
TITLE OF INVENTION: Groups of Borrelia burgd:
TITLE OF INVENTION: Borrelia afzelii That Cau
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
CURRENT FILING DATE: 2000-06-18
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
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; OTHER INFORMATION: OSPC Chimera US-09-596-746-40
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 40
LENGTH: 369
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Best Local Similarity
                            LENGTH: 368
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                           FEATURE:
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87.5%;
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Pred. No. 1.3e-106;
20; Mismatches 25; J
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afzelii That Cause Lyme D
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APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzeili That Cause Lyme Disea
FILE REFERENCE: 2631.1002-00.1
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
SOFTWARE: FastSEQ for Windows Version 4.0
SSEQ ID NO 72
LENGTH: 392
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US-09-596-746-72
; Sequence 72, Application US/09596746
; GENERAL INFORMATION:
; APPLICANT Dattwyler, Raymond J.
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Best Local Similarity
Matches 320; Conser
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                KSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKEL
                                                                             GKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKL 144
                                                                                                    GKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKL 121
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                                                                                                                                                                                                              21;
                                                                                                                                                                                                          Score 1554.5; DB 19;
Pred. No. 5.4e-106;
21; Mismatches 25; I
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APPLICANT: Dattwyler, Raymond J.

APPLICANT: Dykhulzen, Danial

APPLICANT: Dykhulzen, Danial

APPLICANT: Luft, Benjamin J.

APPLICANT: Luft, Benjamin J.

APPLICANT: Maria J.C. Gomes-Solecki

TITLE OF INVENTION: Groups of Borrelia burgdorferi and

TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in

FILE REFERENCE: 2631.1002-001

CURRENT APPLICATION NUMBER: US/09/596,746A

CURRENT FILING DATE: 2000-06-19

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FASTERO for Windows Version A 0
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US-09-596-746A-72
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Best Local (
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SEQ ID NO 72
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TYPE: PRT
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                                                                                                                      A-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCS
                                                                                                                                                                                                       TSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDEL
                                                                                                                                                                                                                                                                   KSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKEL 181
                                                                                                                                                                                                                                                                                                               GKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKL 121
                              ANSVKEL 368
                                                                           EDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEML 361
                                                                                                                                      ATKAIGKKIQONGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCS
                                                        EEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEML
                                                                                                                                                                                      TSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLTSIDEL
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391
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87.2%;
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Pred. No. 5.56
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SOFTWARE: FASTSEQ for SEQ ID NO 38
SEQ ID NO 38
LENGTH: 368
TYPE: PRT
                                                                                                                                                                  US-09-596-746A-38
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Sequence 3B, Application US/09596746A

GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 85.5
Best Local Similarity 86.7
Matches 319; Conservative
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APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelli That Cause Lyme Disease
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US/60/140,042
PRIOR ETLING DATE: 1999-06-18
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                                                                                                                                                                                                                                                                            LANSVKEL 368
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86.7%; Pred. No. 8.1e-105;
tive 20; Mismatches 27;
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US-09-596-746-76
; Sequence 76, Application US/09596746
; GENERAL INFORMATION:
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; ORGANISM: ospC Chimera
US-09-596-746-76
                                ; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for W
; SEQ ID NO 76
; LENGTH: 391
; TYPE: PRT
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CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
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Best Local Similarity
Matches 319; Conserv
                                                                                                                      TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                 APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
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TYPE: PRT
ORGANISM: Artificial Sequence
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Pred. No. 8.1e-105;
Pred. No. 8.2e-27;
                                                                                         Version
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CURRENT APPLICATION NUMBER: US./09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 199-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 76
                                                                                                                                        Query Match
Best Local Similarity
Matches 317; Conserv
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Best Local S
Matches 317
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                    LENGTH: 392
TYPE: PRT
ORGANISM: OSPC Chimera
-09-596-746A-76
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KSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKEL 181
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317; Conserv
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Luft, Benjamin J.
Maria J.C. Gomes-Solecki
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                                                                                                                                        Conservative
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                                                                                                                                    85.1%; Score 1530; DB 19; 86.4%; Pred. No. 3.5e-104; ative 21; Mismatches 27;
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86.4%; Pred. No. 3.5e-104;
71. Mismatches 27;
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SEQ ID NO 26
LENGTH: 374
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Best Local Similarity 83.4%; Pred. No. 3.4e
Matches 312; Conservative 22; Mismatches
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TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
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                                                                                                                                                                                                                                                                                                                  ENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLA 354
                                                                             LASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKI 294
                                                                                                                          ELTSPVVAESPAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETL 240
                                                                                                                                                                                                           KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
                                                             LASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKI
                                                                                                                                            ELTSPIVHG-----NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETL
                                                                                                                                                                                         KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                                                                            IGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTN 119
                                                                                                                                                                                                                                                          IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN
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FastSEQ for Windows Version 4.0
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Luft, Benjamin J.
Maria J.C. Gomes-S
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Seinost, Gerald
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APPLICANT: Selnost, Gerald
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APPLICANT: Selnost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CUURRENT APPLICATION NUMBER: US/09/596,746
CUURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 377
TYPE: PRT
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                                                                             RESULT 15
US-09-596-746A-30
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             Sequence 30, Application US/09596746A
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
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                                                                                                                                                                                                     KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK
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Dykhuizen, Danial
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; Pred. No. 6.2e
23; Mismatches
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.2e-101;
es 34; Indels 9;
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CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER: OF SEO ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 30
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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ORGANISM: Artificial Sequence
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  361
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                                                EKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVE
                                                                                               ELTSPIVHG·······NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEI
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Maria J.C. Gomes-Solecki
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Title:
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Maximum Match 100%
Listing first 45 summaries
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2: //gn2_6/ptodata/2
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US-08-293-603E-15
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Sequence 107, App
Sequence 110, App
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
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Sequence 4, Appli
Sequence 4, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 32, Appli
Sequence 33, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
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       Ω
                                               Query Match 38.9%;
Best Local Similarity 41.5%;
Matches 195; Conservative 49
       7 GKDGNASANSADESVKG-----PNLTEISKKITESNAVVLAVKEVET----LLASID 54
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Result

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9%; Score 5%; Pred. 49; Mis	B235836 B235836 J. J. J. J. J. J. J. J. J. J.	4 US-08-92 4 US-08-97 3 US-08-47 4 US-08-47 4 US-08-47 4 US-08-46 2 US-08-12 1 US-08-46 1 US-08-46 1 US-08-46 1 US-08-46 1 US-08-46 1 US-08-46 1 US-08-92 4 US-08-92 4 US-08-92 4 US-08-91 5 PCT-US-93 5 PCT-US-93 6 US-08-91 6 US-08-91 7 US-08-91 7 US-08-91 8 US-08-91 8 US-08-91
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8; 122; Gaps	for	uence 2, uence 5, uence 5, uence 5, uence 6, uence 4, uence 4, uence 4, uence 4, uence 4, uence 4, uence 1, uence 1, uence 1, uence 1, uence 1,
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US-08-235-836C-107; Sequence 107, Application; Patent No. 6248562
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                                                                                                                                   TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dunn, John J.

APPLICANT: Luft, Benjamin J.

APPLICANT: Dunn, John J.

APPLICANT: Luft, Benjamin J.

APPLICANT: Luft, Ben
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APPLICATION NUMBER: U
FILING DATE: 01-11-93
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CORRESPONDENCE ADDRESS:
                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338 TELEFAX: (516) 282-3729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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CITY: Upton
STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 29-APR CLASSIFICATION: 435
                           TYPE:
                                                                                                                                                                                                                                                                   NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
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ZIP: 11973
TOPOLOGY:
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                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Brookhaven National Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6248562
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 110, Application US/08235836C
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Best Local (
                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 0:
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                      REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin
TITLE OF INVENTION: No. 62
TITLE OF INVENTION: BOrrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 KEYLKGYYLEGTLTAEKTTLYYKEGTYTLSKNISKSGEVSVELNDTDSS--AATKKTAAW 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 KEMLANSVKEL 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 38.8%;
Local_Similarity 47.7%;
                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 11973
                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Upton
STATE: NY
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                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSLLSGAYAISDLIAEKLNVLKNE---ELKEKIDTAKQCSTEFTNKLKSEHAVLGLDNLT 134
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                                                                                                  Bogosian, Margaret C
                                                                                                                                                                                                                                                                                                                                                                                                                        USA
: (516)
(516) 28
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                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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No. 6248562el Chimeric Proteins Comprising
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                                                                                                                                                                     US 08/148,191
                                                                                                                                                                                                                                                    US/08/235,836C
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; Pred. No. 4.1e-45;
43; Mismatches 114;
                                                                  BNL93-28A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptides and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-08-158-353-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 466 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Padula
                            FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CRITCII, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UCT9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEPAX: 617-861-9540
TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELTSPIVHGNNSGKDGNTSA----NSADESVKGPNLTEISKKITESNAVVLAVKEIETLL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEETN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SK-DKSSTEEKFNEKGE----VSEKIITRADGTRLEYTGIKSDGSGKAKEVL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATVDKLELKGTSDKNNGSGVLEGVKADKSKVKLTISDDLGQTTLEVFKEDGKTLVSKKVT
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                                                                                                                                                                                                                                                                          Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steven J.
Methods for Diagnosing Early Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disease
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                                                                                  UCT93-05
                                                                                                                                                                                                                                                                                                                                                                                             Smith & Reynolds,
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                                                                                                                                                                                                                        Version #1.25
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; TYPE: amino ac
; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: p
US-08-158-353-2
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; ORGANISM: Borrelia burgdorferi
US-09-196-293-15
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                                                                                                                           Query Match
Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 15
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EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER FILING DATE: 1994-03-10
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1990-06-19
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER APPLICATION NUMBER: DE P39 42 728.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Motz, Manfred
APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettlina
APPLICANT: Preac-Mursic, Vera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Active proteins from Borrelia TITLE OF INVENTION: burgdorferi FILE REFERENCE: 738.001US2
                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1989-12-22
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER FILING DATE: 1990-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fuchs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/196, 293
                                                                                                                                                                                                                                                                   LENGTH:
                             249
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               KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL 308
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                                                                                                                                                35.8%;
75.6%;
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72.9%;
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                                                                                                                              Score 644.5; DB 4;
Pred. No. 1.6e-41;
"" matches 28;
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Pred. No. 1.7e-42;
                                                                                                                                                                  Length 209;
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US 08-235-836C-30
; Sequence 30, Application US/08235836C
; Patent No. 6248562
; GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice 0.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Padula, Steven J.
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 7
                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        139
                                                                                                                                                                                                                       309 EGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 KEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL
                                                                                                                                                                                                                                                                                                        249 KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL 308
                                                                                                                                                                                                                                                                        90
                                                                                                                                                                                                                                                                                                                                            20 NNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGK 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                        KIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETFTNKL
                                                                                                                                                                                                       KEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08158353
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Dunn, John J.
Luft, Benjamin J.
VENTION: No. 6248562el Chimeric Proteins Comprising
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75.6%;
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; Pred. No. 1.6e-41
15; Mismatches 2
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; MOLECULE TYPE:
US-08-235-836C-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: FUCHS, RENATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                       APPLICANT: FUCHS, RENATE
APPLICANT: WILSKE, BETTINA
APPLICANT: PREAC-MURSIC, V
APPLICANT: MOTZ, MANFRED
APPLICANT: SOUTSCHECK, ERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
TELEPHONE: (516) 282-3729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PATERILL.
SOFTWARE: PATERILL DATA:
CURRENT APPLICATION NUMBER: US/08
APPLICATION 29-APR-1994
175
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ATTORNEY/AGENT INFORMATION:
NAME: BOGGSIAN, MARGARET C.
                                                                                                                                                                                                                                         TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS TITLE OF INVENTION: FROM BORRELIA BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                     CITY:
                                                                                                  STREET:
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COUNTRY:
                                    STATE:
                                                                                                                                      ADDRESSEE:
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                                NEW YORK
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PREAC-MURSIC, VERA
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75.0%;
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Pred. No. 3.9e-41;
Pred. No. 3.9e-41;
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; PUBLICATION INFORMATION:
US-08-209-603E-15
                                                                                                                                                                                                    RESULT 9
US-08-031-295-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                Sequence 2, Application US/08031295 Patent No. 5530103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                          GENERAL INFORMATION:
APPLICANT: LIVEY, Ian
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AN
TITLE OF INVENTION: PREVENTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/EFYV/-
APPLICATION NUMBER: US 07/862,;
FILING DATE: 19-JUN-1992
ATTORNEY_AGENT INFONMATION:
NAME: ROBINSON, WILLIAM R.
NAME: ROBINSON, WILLIAM R.
NAME: ROBINSON, WILLIAM R.
NAME: ROBINSON, WILLIAM R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: N/A
ANTI-SENSE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
IMMEDIATE SOURCE:
LIBRARY: DSM 5662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: ATAT - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CORRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FL
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                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                           139
                                                                                                                                                                                                                                                                                         309 EGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL 368
                                                                                                                                                                                                                                                                                                                                                                              249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/209,603E FILING DATE: 10-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                             20 NNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVLEVEALLSSIDEIAAKAIGK 79
                                                                                                                                                                                                                                                                                                                                            KIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETFTNKL
                                                                                                                                                                                                                                                                                                                                                                           KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL 308
                                                                                                                                                                                                                                                                       KEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N/A
                                                                           METHOD AND COMPOSITION FOR THE PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.5%; Score 637.5; DB 4; 75.0%; Pred. No. 5.5e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 07/862,535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid analysis N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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US-08-031-295-2
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                                                                                                                                                                                                                                                                                         200 L 200
                           STREET:
                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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Sequence 2, Application US/07903580 Patent No. 6221363
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Best Local Similarity
Matches 127; Conserv
                         APPLICANT: LIVEY, IAN
APPLICANT: DORNER, Freidrich
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: PREVENTION
TITLE OF INVENTION: PREVENTION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: AMINO ACID
                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/1
FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/2
FILING DATE: 11-TUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-BOS MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              140 LAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANSVKE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 NNSGKDGNT-SANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIG 247
                                                                                                                                                                                                                                                                                                                                                                                                                      308 LEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKE 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 NNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATKAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington, D.C.
E: Foley & Lardner
1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : (202)672-5300
(202)672-5399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.4%; Score 600.5; DB 1; 70.2%; Pred. No. 3.4e-38; tive 20; Mismatches 33;
                                                                                   PREVENTION
                                                                                                       METHOD AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 07/727,245
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  Suite 500
                                                                                 COMPOSITION FOR OF LYME DISEASE
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

COUNTRY:

Virginia

22313-0299

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                                                                                                                                                                           Sequence 4, Application US/08158353
Patent No. 5620862
GENERAL INFORMATION:
APPLICANT: Padula, Steven J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,245
FILING DATE: 11-JUL-1991
ATTORNEY/ACENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
                              STREET: 'IWC .
CITY: Lexington
CTATE: MA
TISA
                                                                                                       NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           368 L 368
                                                                                                                                                                                                                                                                                                                                                                   140 LAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANSVKE 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELLEFAX: (... 899149
                  COUNTRY: UZIP: 02173
                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 212 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATKAIG 79
                                                                          E: Hamilton, Brook, Two Militia Drive
                                                                                                                                    Padula, Steven J.

VENTION: Methods for Diagnosing Early Lyme
VENTION: Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.4%; Score 600.5; DB 4; Length 212; 70.2%; Pred. No. 3.4e-38;
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                                                                                        Smith & Reynolds,
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US-08-235-836C-34
; Sequence 34, Application US/08235836C; Patent No. 6248562
; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: UC:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
                                                                                                                                                                                                                        Aub...
STREET:
Opton
NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 VKELTSPVV 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 THKLKSEHAVLGLDHLTDDHAQRAILKKHANKDKGAAELEKLFKAVEHLSKAAQDTLKHA 177
                                                                                                                                                                                    COUNTRY: USA
ZIP: 11973
                                                                                                                                                                                                                                                                       ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 AIGKKI-GNNGLEANOSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTEF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKK 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130;
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                                                                                                                                                                                                                                                                                                                                            No. 6248562el Chimeric Proteins Comprising
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68.8%; Pred. No. 2.70
tive 20; Mismatches
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Gaps

APPLICATION NUMBER: US 01 FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:

US 08/148,191

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APPLICANT: SOLUSIONES, ETWIN
APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.001US2
CURRENT FILING DATE: 1998-11-19
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER FILING DATE: 1994-03-10
EARLIER FILING DATE: 1992-06-19
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1998-12-22
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-06-13
EARLIER FILING DATE: 1990-06-13
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Best Local Similarity
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                                            SOFTWARE: FastSEQ
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 61837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (516) 282-3729 INFORMATION FOR SEQ ID NO:
                                                                                   NUMBER OF SEQ ID NOS:
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 AIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNYLKN-EELKEKIDTAKQCSTEF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
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amino acid
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                                                                 Windows Version 4.0
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Patent No. 6
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Best Local Similarity
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                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP90/02282
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/862,535
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9217-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                  TELEFAX: (212) 557-5635 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT4T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version
SOFTWARE: ASCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PRITITLE OF INVENTION: FROM BORRELIA BURGDORFERI NUMBER OF SEQUENCES: 15
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197 VKELTSPVV
                               HYPOTHETICAL:
ANTI-SENSE: 1
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               FRAGMENT TYPE:
                                                                                          MOLECULE TYPE:
                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 99 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 AIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTEF 117
                                                                DESCRIPTION:
                                                                                                       TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                               ENGTH:
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6248538
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RESULT 15
US-08-235-836C-36
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; ORIGINAL SOURCE:
US-08-209-603E-11
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Best Local Similarity 68.3
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                 APPLICATION NUMBER: US/08/
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret C
                                  TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                              NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
   SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                STREET:
CITY: Upton
STATE: NY
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POSITION IN GENOME: N/A
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                                                                                                                                                                                                                                                                                                                                                                      ZIP: 11973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Brookhaven National Laboratory
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amino acids
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                                                                                                                                                                                    US 08/148,191
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                                  36:
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-235-838C-36
                                                                                                                                                                                                                                Query Match 31.3%;
Best Local Similarity 62.6%;
Matches 117; Conservative 3
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                                                  134 KLKDSHAELGIQSVQDDNAKKAILKTHGTKDKGAKELEELFKSLESLSKAAQAALTNSVK 193
194 ELTNPVV 200
                          180 ELTSPIV 186
                                                                120 KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
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                                                                                                           IGKKIKNDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSEKFTT 133
                                                                                                                                                                                                                              34; Mismatches
                                                                                                                                                                                                                                           Score 563; DB 4; Length 207; Pred. No. 2.2e-35;
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Search completed: March 18, 2002, 09:55:35 Job time: 348 sec THIS PAGE BLANK (USPTO)

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Result
No.
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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	outer surface			outer surface	outer surface	outer surface										

ALIGNMENTS

outer surface protein C precursor - Lyme disease spirochete C;Species: Borreila burgdorferi (Lyme disease spirochete) C;Date: 12-Aug-1996 *sequence_revision 12-Aug-1996 *text_change 21-Jul-2000 C;Accession: I40142; S70283 R;Stevenson, B.; Bockenstedt, L.K.; Barthold, S.W. Infect. Immun. 62, 3568-3571, 1994

A;Title: Expression and gene sequence of outer surface A;Reference number: I40142; MUID:94314484 A;Accession: I40142

protein

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of Borrelia burgdorf

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Q.

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Residues: 1-209 < RES>

A; Molecule type: DNA

RESULT I40142

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A; Notatus. ......
A; Molecule type: DNA
A; Residues: 19-209 <LIV>
A; Cross-references: EMBL:L42894; NID:g858722; PIDN:AAB37002.1; PID:g1695219
A; Cross-references: Strain 28691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U04240; NID:g2314877; PIDN:AAC45588.1; PID:g434658 R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995 Mol. Microbiol. 18, 257-269, 1995 A;Title: Evidence for lateral transfer and recombination in OspC variation A;Reference number: S70255; MUID:96296448
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C;Superfamily: Lyme disease spirochete surface protein
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RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          1 MACNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKA 60 ::|||||||||||||||||||
                                                                                                                                                                      LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE 180
                                                               LTSPIV
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Pred. No. 4.4e-36;
2; Mismatches 0
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C;Superfamily: Lyme disease spirochete surface protein
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A;Title: Humoral immune response to outer surface protein
Apperence number: I40153; MUID:94314437
                                                                                                                                                                                                                                                                                                                                                                                                       outer surface protein C - Lyme disease spirochete (fragment) C:Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change C:Accession: I40153
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outer :
C;Spec
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R;Live
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R;Livey, I; Gibbs, C.P.; Schuster, R.; Dorner, F.

Mol. Microbiol. 18, 257-269, 1995

A;Title: Evidence for lateral transfer and recombination
A;Reference number: S70255; MUID:96296448

A;Accession: S70287
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                                                                                                                                                                       Query Match
Best Local Similarity
Matches 178; Conserv
                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                              Peference number: 140153; MUID:94314437 Cession: 140153 Cession: 140153 Actus: preliminary; translated from GB/EMBL/DDBJ Molecule type: DNA
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Matches 180;
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;Species: Borrelia burgdorferi (Lyme disease spirochete)
;Date: 12-Feb_1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000
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IQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLE 309
                                                                                                           NSGKGGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGKK 60
                                                      KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL
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Pred. No. 2.4e-34;
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6e-35;
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C;Accession: I40104; S54184
C;Accession: M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, J. Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrelia burgdorferi outer: A;Reference number: I40104; MUID:95286481
                                                                                                                                                                                                                                                                                                                                                              A;Gene: ospC
C;Superfamily:
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A; Residues: 1-178 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outer surface protein C - Lyme disease spirochete (strain 272) (fragment) C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000 C;Accession: I40104; S54184
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A; Residues: 1-178 < RES>
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A;Title: Evolution of the Borrelia burgdorferi outer surfa A;Reference number: I40104; MUID:95286481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outer surface protein C - Lyme disease spirochete (strain MUL) (fragment) C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000 C;Rtcession: I40125; S54195
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 NTSANSADESVKGPNLTEISKKITESNAVVLAVKBIETLLASIDELATKAIGKKIQQNGG 255
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                      GIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL
                                                                                                     LAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQL
                                                                               LAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLTEKIENAKRCSEDFTKKLEGEHAQL
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                                                                                                                                                                                                                                                               170;
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                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                       Lyme disease spirochete surface protein
                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                          45.8%;
98.3%;
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                                                                                                                                                                                                                                                      Score 823; DB 2;
Pred. No. 1.7e-32;
1; Mismatches 2
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Pred. No. 1.2e-32;
0; Mismatches 2
                                                                                                                                                                                                                                                                                           Length 178
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outer surface protein C precursor - Lyme disease spirochete (strain PKa)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
A;Variety: strain PKa
C;Date: 15-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-May-2000
C;Accession: S69927; S72669
R;Jauris-Heipke, S.; Liegl, G.; Preac-Mursic, V.; Roessier, D.; Schwab, E.; Soutschek,
J. Clin. Microbiol. 33, 1860-1866, 1995
A;Title: Molecular analysis of genes encoding outer surface protein C (OspC) of Borreli A;Reference number: I40047; MUID:95395018
A;Accession: S69927
                                                                                                                                                                                                                                                                                                        A:Molecule type: DNA
A:Residues: 1-124,'D',126-139,'E',141-210
A:Cross-references: EMBL:X69589
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A;Molecule type: DNA
A;Residues: 1-178 <RES>
A;Cross-references: EMBL:X84782; NID:g793815; PIDN:CAA59253.1; PID:g793816
C;Superfamily: Lyme disease spirochete surface protein C
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A; Accession: I40124
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R;Thelsen, M.; Borre, M.; Mikkelsen, M.J.; Mikkelsen, J. Bacter.ol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrelia burgdorferi outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outer surface protein C - Lyme disease spirochete (strain KIPP) (fragment) C:Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 02-Nug-1996 #sequence_revision 02-Nug-1996 #text_change 26-May-2000
                                                                                                                                                                                                                                            C; Superfamily: Lyme disease spirochete surface protein
                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S72669
A; Accession: S72669
                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library,
                                                                                                                                 Query Match
Best Local S
Matches 137
                                                                                                                                                                                                                                                                                             Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: nucleic acid sequence not Molecule type: DNA esidues: 1-210 <JAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Experimental source: strain PKa
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249 KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL
                                                                                   189 NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGK 248
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                                                                                                                                    Local Similarity
les 137; Conserv
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                                            NNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGK 79
                                                                                                                                 Conservative
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                                                                                                                                                  36.1%;
76.1%;
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89.08;
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                                                                                                                                    14;
                                                                                                                               Score 648.5; DB 2;
Pred. No. 3.2e-24;
4; Mismatches 28;
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Pred. No. 1.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                              February 1994
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FEMS Microbiol. Lett. 124, 367-372, 1994
A;Title: Expression and sequence of outer
A;Reference number: I40143; MUID:95154673
A;Accession: I40145
A;Status:
                                                                                                                                                                                                                                                          outer surface protein C - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Decies: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13:Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000 C;Accession: G70218; I40269; S37726; S70281 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatture 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outer surface protein C precursor - Lyme disease spirochete C:Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change C:Accession: I40145
R;Fukunaga, M.; Hamase, A.
J. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence
A;Reference number: I40269; MUID:96025162
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C;Superfamily: Lyme disease spirochete surface
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                                                                                                                                                                            A;Title: Genomic sequence of a Lyme disease spirochaete, A;Reference number: A70100; MUID:98065943 A;Accession: G70218
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A; Residues: 1-211 <RES>
                                                                                                                                                             A;Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                          Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLITQKLGGLKNEELKEKIAAVKKCSEEFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL
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72.3%;
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                                                                                                   NID: g3253098;
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Pred. No. 4.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                     PIDN: AAC66329.1;
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                                                                                                                                                            C; Superfamily: Lyme disease spirochete surface protein
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A;Residues: 1-193 <LIV>
A;Cross-references: EMBL:L42898; NID:g858729;
A;Experimental source: strain 25015
                                                                                                                                                                                                                                                                                                  R;Livey, I.; Glbbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in
A;Reference number: S70255; MUID:96296448
A;Accession: S70279
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
S70279
                                                                                                                                                                                       A; Gene:
                                                                                                                                                                                                                                                                               A; Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684 R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Med. Microbiol. Immunol. 182, 37-50, 1993 A;Title: Genetic heterogenity of the genes coding for the outer surface A;Reference number: S37726; MUID:93268136 A;Accession: S37726
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C; Superfamily:
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A; Residues: 1-210 <JAU>
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Best Local S
Matches 136
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                                                                                    Matches 135;
                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                   Genetics:
                                                                                                                                                                                                                                                                                                                                                                                  r surface protein C - Lyme disease spirochete ecies: Borrelia burgdorferi (Lyme disease spirochete) Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change Accession: S70279
                                                                                                                                                                                                                                                                                                                                                                                     Accession:
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Cross-references: EMBL:L42887; NID:g858715;
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                             3 CNNSGKDGN-ASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKAI 61
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                                                                                    Conservative
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72.6%;
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75.6%;
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                                                                             Score 642; DB
Pred. No. 5.8e
16; Mismatches
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Pred. No. 4.9e-24;
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                                                                             DB 2; ]
5.8e-24;
les 33;
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-210 <RES>
A;Cross-references: EMBL:U04281; NID:g434663; PIDN:AAC43297.1; PID:g434664
R;Livey, I; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
                                                                                                                                             R:Stevenson, B.; Barthold, S.W.
FEMS Microbiol. Lett. 124, 367-372, 1994
A:Title: Expression and sequence of outer surface
A:Reference number: I40143; MUID:95154673
A:Accession: I40144
                                                                                                                                                                                                                                                            outer surface protein C precursor - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_che C;Accession: I40144; S70282
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R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, Mol. Microbiol. 18, 257-269, 1995

A;Title: Evidence for lateral transfer and recor A;Reference number: S70255; MUID:96296448

A;Accession: S70280

A;Status: nucleic acid sequence not shown
                                                                                                                              A; Status: preliminary;
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C;Superfamily: Lyme
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A; Residues: 1-193 <LIV>
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Best Local
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76.2%;
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Pred. No. 7.2e
16; Mismatches
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.2e-24;
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outer surface protein C precursor - Lyme disease spirochete (strain PBre) C:Species: Borrella burgdorferi (Lyme disease spirochete)
A:Variety: strain pBre
C:Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000
C:Accession: S69918: S72674; I40103
R:Jauris Helpke, S.; Liegl, G.; Preac-Mursic, V.; Roessler, D.; Schwab, E.;
J. Clin. Microbiol. 33, 1860-1866, 139-Mirsic Victorial Communication of S6918
A:Reference number: I40047; MUID:95395018
A:Accession: S69918
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A;Residues: 19-210 <LIV>
A;Cross-references: EMBL:L42893; NID:g858721;
A;Experimental source: strain 297
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A;Recession: $70282
A;Status: nucleic acid sequence not shown
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A; Residues: 1-152, 'E', 154-211 <ROE>
A; Cross-references: EMBL: X81522; NID: g872021;
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A; Residues: 1-211 <JAU>
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Best Local Similarity
Matches 134; Conserv
                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                         ; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        the the EMBL Data Library, Reference number: S72674
                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference number:
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EGEHAQLGIENVTDENAKKAILITDAA-KDKGAAELEKLFKAVENLAKAAKEMLANSVKE
                                                                                                                                                            NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGK 248
                                                          KIKNDGSLGDEANHNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFSTKL
                                                                                                 KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL 308
                                                                                                                                        NNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELA-KAIGK 78
                                                                                                                                                                                                                     Conservative
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Pred. No. 8.4
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                                                                                                                                                                                                                                                                                                                                                                             PIDN:CAA57242.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:CAA57242.1;
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C;Accession: I40268
R;Margolis, N.; Hogan, D.; Cieplak, W.
Gene 143, 105-110, 1994
A;Title: Homology between Borrelia burgdorferi OspC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Theisen, M.; Frederiksen, B.; Lebech, A.M.; Vuust, J.; Ha
J. Clin. Microbiol. 31, 2570-2576, 1993
A;Title: Polymorphism in ospC gene of Borrelia burgdorferi
A;Reference number: 140105; MUID:94075528
A;Accession: 140108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outer surface protein C - Lyme disease spirochete (strain DK7) (fragment) C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-20: C;Accession: I40108; S34176
                                                                                      A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
                                                                                                                                                                                                                     A; Reference number: I40268;
A; Accession: I40268
                                                                                                                                                                                                                                                                                                                                 outer surface protein C precursor - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
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C;Superfamily: Lyme disease spirochete surface protein
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A;Residues: 1-203 <RES>
A;Cross-references: EMBL:X73625; NID:g313275; PIDN:CAA52004.1; PID:g313276
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A; Residues: 1-211 <RES>
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Query Match 34.9%;
Best Local Similarity 72.8%;
Matches 131; Conservative 1
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Best Local Similarity
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Pred. No. 1.3e-23;
 Score 627; DB 2;
Pred. No. 3.3e-23;
6; Mismatches 33;
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189 NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGK 248

Search completed: March 18, 2002, 09:56:49 Job time: 372 sec

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Title:
Perfect score:
Sequence:
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2: /cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

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sequence
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58883, Appli

58883, Ap

13080, A

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13080, A

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TION: hiesen, Marianne J. elsen, Michael lm, Arne tergaard, Soren TION: Novel OspC-deri 149-666P ATION NUMBER: US/09/9 ATION NUMBER: 09/180,08 ATE: 1999-05-13 ION NUMBER: PCT/DK97/ ATE: 1997-05-02 ID NOS: 40 ntin Ver. 2.1 relia burgdorferi relia burgdorferi larity 76.2%; Pred Conservative 16; M NTSANSADESVKGPNLTEISK NTSANSADESVKGPNLTEISK LAVENGHNGTLLAGAYTISK:	168865555555555555555555555555555555555
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APPLICANT: Ostergaard, Soren
ITILE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR APPLICATION NUMBER: PCT/DK97/00203
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
                                                                                                   ; ORGANISM: Borrelia garinii
US-09-974-992-3
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         Matches 118;
                       Query Match
Best Local Similarity
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Best Local Similarity 68.8%;
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CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
                                                                                                                                      LENGTH: 207
TYPE: PRT
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TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 VKELTSPIV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 AIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTEF 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKELTSPVV 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09974992
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                                                                                                                                                                                                                                                                                                                                                                                                                   Theisen, Michael
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       Conservative
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31.5%; Score 567; DB 6; I
63.1%; Pred. No. 7.8e-32;
93. Mismatches 32;
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Pred. No. 2.7e-33;
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                                     Length 207;
   Indels
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 93; Conserv
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LENGTH: 837
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SOFTWARE: FastSEQ for Window
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE; ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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218 AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN 272
                                                110
                                                                                          160
                                                                                                                                                              100 NHNLEVAKQNANTAIDGLTSLNGPQKAKLKEQVGQATTLPNVQTVRDNAQTLNTAMKGLR 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
                                                                                                                                                                                                           4 NNSGKDGNASANSADE----SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
                                       AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE 164
                                                                                 DSIANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
                                                                                                                       DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE----KLNVLKNEELKEKIDT 109
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23.1%; Pred. No. 0.00026;
ative 77; Mismatches 154;
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US-10-072-851-5883
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Best Local Similarity 23.1
Conservative
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-10-072-851-5883
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                                                                                                                                                                                                  160 DSIANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
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                                                                                                                                                                                                                         54 DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE----KLNVLKNEELKEKIDT 109
                                                                                                                                                                                                                                                                                                             4 NNSGKDGNASANSADE----SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI----
        AVVLAVKEIETLLASIDELATKAIGKKIQQNGGLAVEAG------HNGTLLAGAY 271
                                                                                                                          AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN
                                                                                                                                                          AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE 164
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                                                NADALNTAMTNLKNGIQD-----QNTIKQG-VNFTDADE-----AKRNAYTN
                                                                                    NLS--KAAQDTLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESN 222
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Boone, Charles
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Yamamoto, Robert T.
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Zyskind, Judith W.
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Zamudio, Carlos
Haselbeck, Robert
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23.1%; Pred. No. 0.00026;
tive 77; Mismatches 154
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SEQ ID NO 13080
LENGTH: 875
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
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223 AVVLAVKEIETLLASIDELATKAIGKKIQQNGGLAVEAG-----
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                                                                                                                          255 AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN
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                                                                                                                                                                                                                                 DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE----KLNVLKNEELKEKIDT 109
                                                                                                                                                                                                                                                                                                                 NNSGKDGNASANSADE----SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI---- 53
                                              NADALNTAMTNLKNGIQD------QNTIKQG-VNFTDADE---
                                                                                                                                                            AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE 164
                                                                                                                                                                                                    DSIANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
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                                                                                    NLS--KAAQDTLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESN
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Xu, H. Howard
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US-10-072-851-13080
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US-10-072-851-13080
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NUMBER OF SEQ ID NOS: 15811
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TYPE: PRT
                       397 TTAKNALNNLTSINNAQKEALKSQIEGATTVAGVNQVSTTASELNTAMSNLQNGINDEAA
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                                                              272 TISKLITOKLDGLKNSEK--LKEKIENAKK---CSEDFTKKLEGEHAQLGIEN-VTDENA 325
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nes 93; Conserv
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                                                                                                                                                AVVLAVKEIETLLASIDELATKAIGKKIQQNGGLAVEAG-----
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                                                                                                                                                                                                                                                                                                               AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE
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                                                                                                         AVTQA-------EQILNKAQGPNTSKDG---VETALENVQRAKNELNGNQNVANAK
                                                                                                                                                                                                                                  NLS--KAAQDTLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESN 222
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Ohlsen, Kari L
Zyskind, Judith W.
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Yamamoto, Robert T.
Roemer, Terry
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US-09-708-427-15044
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: LCCATION: 1..1304
: OTHER INFORMATION: Ceres Seq.
US-09-708-427-15045
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US-09-708-427-15045
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Sequence 15044, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,42
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LENGTH: 1304
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Best Local :
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
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                                                                                                                                                                                                                                                                      326 KKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANS 364
                                                                                                                                                                                                                                                                                                                                                                                                 302 QLAELNHVLHETKSDNAAQKEKIELLEKTIEAQRTDLEEYGRQV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLGSKEEKEAIE-----GNEIVSKLKSE-----IELLRGELEKVSILESSLKEQEGLVE
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                                                                                                                                                                                                                                                                                                               ----CIAKEEASKLENL--VESIKSELEISQ---EEKTRALDNEKAATSNIQNLLDQRT
                                                                                                                                                                                                                                                                                                                                                      LAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQL-GIENVTDENA 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEKL----FKAVENLSKAAQDTLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKG--P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ELKEKIDTAKQCSTEFTNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLSTTEEL-----QRVKHELSMTADAKNKALSHAEEATKIAEIHAEKAEILASELGRLK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEKLKEALAAQKRAEESFEVEKFRAVELEQAGLEAVQKKDVTSKNELESIRSQHALDISA 144
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91; Conserv
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NUMBER: US/09/708,427
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Pred. No. 0.0012;
00; Mismatches 136; Indels
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NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15044
LENGTH: 1313
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                 TITLE OF INVENTION: Identification of Essential Ge TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITA,011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727
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Best Local S
Matches 91
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: 1..1313
OTHER INFORMATION: Xaa is any amino acid
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                                                                                                                                                                                                                                      Xu, H. Howard
                                                                                                                                                                                                                                                                                              Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                      Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                     Ohlsen, Kari L.
Zyskind, Judith W.
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APPLICANT: Jiang, Bo
APPLICANT: Jiang, Bo
APPLICANT: Boone, Charles
APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying th
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA 028A
CURRENT APPLICATION NUMBER: US/10/072,851
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US-10-072-851-5835
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Best Local S
Matches 94
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5835
LENGTH: 2434
                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5835,
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APPLICANT:
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Carr, APPLICANT: Xu, I
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les 94; Conserv
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                                                                                                                                                                            Yamamoto, Robert T. Roemer, Terry
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Zyskind, Judith W.
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Zamudio, Carlos
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US-10-072-851-5835
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LENGTH: 2434
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                                                            PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
                                                                                                        PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                 PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/267, PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                            PRIOR FILING DATE: 2000-03-21
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(PPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quence 12996, Application US/09815242
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                                                                                                                                                                                                                                                                                                                                                          Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                           Wall, Daniel
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60/257,931
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            APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12996
SEQ ID NO 12996
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Best Local :
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                                                                                                                                                                                                                                                       Yamamoto, Rowerson, Terry
                                                                                                                                                                                                                                                                                                                                Wall, Daniel
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Zamudio, Carlos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    H. Howard
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                                                                                                                                                                                                                                                                                       Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gordon
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. NUMBER OF SEQ ID NOS: 36

. SOFTWARE: Patentin Ver. 2.0

. SEQ ID NO 8

. LENGTH: 1765

. TYPE: PRT

. ORGANISM: Homo sapiens

US-10-037-182-8
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US-10-037-182-8
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GENERAL INFORMATION:
APPLICANT: Tryggyason, Karl
APPLICANT: Doi, Masayuki
APPLICANT: Thyboll, Jill
TITLE OF INVENTION: Recombinant Laminin 10
FILE REFERENCE: 99-274-F
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Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                        Query Match
Best Local
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,449
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/279,282
PRIOR FILING DATE: 2001-03-28
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1444 VSEAKLRAD------EAKQSAEDILLK----TNATKEKMD-KSNEELRNLIKQIRN 1488
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                                                                                                                                                                                        Match 9.4%;
Local Similarity 24.6%;
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                                                                                                                           2 ACNNSGKDG-NASANSADESVKGPNLTEI-----SKKITESNAVVLAVKEVETLLAS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAKNALNNLTSINNAQKEALKSQIEGATTVAGVNQVSTTASELNTAMSNLQNGINDEAA 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSIANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T 1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE----KLNVLKNEELKEKIDT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHNLEVAKQNANTAIDGLTSLNGPQKAKLKEQVGQATTLPNVQTVRDNAQTLNTAMKGLR 1540
                                       IDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQ 112
                                                                                 SCSETECGGPNCRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLSALAEVEQLSKM 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKAI-LITDAAKDKGAAELEKLFKAVENLAKAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVVLAVKEIETLLASIDELATKAIGKKIQQNGGLAVEAG------HNGTLLAGAY 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLS--KAAODTLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESN 222
                                                                                                                                                                       102;
                                                                                                                                                                       Conservative
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                                                                                                                                                                  Score 168.5; DB 7;
Pred. No. 0.0023;
1; Mismatches 160;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Therapeutic and Diagnostic Applications TITLE OF INVENTION: of Laminin and Laminin-Derived Protein FILE REFERENCE: PROTEO, P03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Swissprot P07942
DATABASE ENTRY DATE: 1988-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/938,275
CURRENT FILING DATE: 2001-08-16
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1673 EKVV---YTVKQSAEDVKKTLDG-ELDEKYK-KVENLIAKKTEESADARRKAEMLQNEAK 1727
                                                                                                                                                                                     1570 RAEM--LLEEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIK------QADEDI 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113
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                                                                                                                                                                                                                                                                                                                            113 CSTEFTNKLKSEHAVLG------LDNLTDDNAQRA-----ILKKHANKDKG 152
                                                                                                                                                                                                                                                                                                                                                                                                                    53 IDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ACNNSGKDG-NASANSADESVKGPNLTEI-----SKKITESNAVVLAVKEVETLLAS 52
                                         GTLLAGAYTISKL---ITQKLDGLKNSEKLKEKIEN--AKKCSEDFTKKLEGEHAQLGIE 318
                                                                                                                               KGPN--LTEISKKITESNAVVL-AVKEIETLLASIDELATKAIGKKIQQNGGLAVEAGHN 263
                                                                                                                                                                                                                                                                                                                                                                          VSEAKLRAD---
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                                                                                          QGTQNLLTSIESETAASEETLFNASQRISELERNVEELKRKA-----AQNSG---EAEYI 1672
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1798
1 MACNNSGKDGNASANSADES......AVENLAKAAKEMLANSVKEL
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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SEQUENCE FROM N.A. STRAIN=ATCC 35210 / B31; STRAIN=ATCC 35210 / B31; STRAIN=ATCC 35210 / B31; MEDLINE=98065943; PubMed=9403685; MEDLINE=98065943; PubMed=9403685; Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Fraser C.M., Casjens S., Huang W.M., Dodson R., Hickey E.K., Gwinn M., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb JF., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,	SEQUENCE FROM N.A. STRAIN=ATCC 35210 / B31; MEDLINE=96025162; PubMed=7494039; Fukunaga M., Hamase A.; "Outer surface protein C gene sequence analysis of Borrelia burgdorferi sensu lato isolates from Japan."; J. Clin. Microbiol. 33:2415-2420(1995).	SEQUENCE FROM N.A. STRAIN-ATCC 35210 / B31; S	SEQUENCE FROM N.A. STRAIN=ATCC 35210 / B31; MEDLINE=9323932; PubMed=8478108; Wilske B., Preace-Mursic V., Jauris S., Pradel I., Soutschek E., Schwab E., Wanner G.; "Immunological and molecular polymorphisms of OspC, an immunodominant major outer surface protein of Borrelia burgdorferi."; Infect. Immun. 61:2182-2191(1993).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-ATCC 35210 / B31; MEDLINE-93268136; PubMed-8098841; Jauris-Heipke S., Fuchs R., Motz M., Preac-Mursic V., Schwab E., Will G., Wilske B.; "Genetic heterogenity of the genes coding for the outer surface protein C (OspC) and the flagellin of Borrelia burgdorferi."; Med. Microbiol. Immunol. 182:37-50(1993).	RESULT 1 OSC1_BORBU STANDARD; PRT; 210 AA. ID OSC1_BORBU STANDARD; PRT; 210 AA. AC Q07337; DT 15-DEC-1998 (Rel. 37, Last sequence update) DT 20-AUG-2001 (Rel. 40, Last annotation update) DE QUTER SURFACE PROTEIN C PRECURSOR (PC). GN OSPC OR BBB19. OS BORTelia burgdorferi (Lyme disease spirochete). OG Plasmid 1p54. OX NCBI_TaxID=139; RN (1]	

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Matches 136
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EMBL; U01894;
EMBL; D49497;
    "Molecular analysis and expression encoding a 22 kDa protein (pC) in I Mol. Microbiol. 6:503-509(1992).
                                                                                                             Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; S
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Q08137;
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Soutschek E.;
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ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Plasmid; Antigen;
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                                              Preac-Mursic V.,
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P32778;
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STRAIN-SSP, HS1 SEROTYPE 24;
STRAIN-SSP, HS1 SEROTYPE 24;
MEDLINE-93133110; PubMed=1484486;
Restrapo B.I., Kitten T., Carter '
"Subtelomeric expression regions'
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J. Clin. Microbiol. 31:2570-2576(1993).
-i- FUNCTION: NOT KNOWN, MAJOR IMMUNODOMINANT PROTEIN.
-i- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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STRAIN=DK26;
MEDLINE=94075528; PubMed=8253951;
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                                                                                             Spirochaetales;
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                                                                                                                                                                  (Rel.
                                                                                                                                                                                             (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                  el. 27, Created)
el. 27, Last sequence up
el. 28, Last annotation
OUTER MEMBRANE LIPOPROT
                                                                                                                                                                                                                       STANDARD;
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212
19
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68.8%;
                                                                                                                                                     MEMBRANE LIPOPROTEIN
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                                                                                              Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Plasmid; Antigen.
BY SIMILARITY.
OUTER SURFACE PROTEIN C;
N-ACYL DIGLYCERIDE (BY SIMILARITY).
C206C231FBF2E7D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.70
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                       PRT;
 of Bo
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No. 1.7e-20;
 Borrelia hermsii linear
                                                                                                                                                                               update)
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                                                                                                                                                       PRECURSOR
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               Barbour A.G.;
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Best Loc
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01-JUL-1993
01-FEB-1994
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIPID
                                    are
                                               Restrepo B.I., Kitten T., Carter "Subtelomeric expression regions
                                                                       STRAIN-SSP. HS1 SEROTYPE 3;
MEDLINE-93133110; PubMed-1484486;
                                                                                                                                                              Borrelia
                                                                                                                                                                                                                                          Q02448;
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                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                      Bacteria; Spirochaetales;
                                                                                                                                                                                        VARIABLE
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         highly polymorphic.";
. Microbiol. 6:3299-3311(1992).
FUNCTION: SERVES TO AVOID THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  highly polymorphic.";
Microbiol. 6:3299-3311(1992).
FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY:
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 ONE SURFACE
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(Rel. 26,
(Rel. 28,
JOR OUTER N
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EXPOSED VMP
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, Last annotation update)
MEMBRANE LIPOPROTEIN 3 P
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                                                                                                                                      Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 346; DB Pred. No. 1.2e 0; Mismatches
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                                                                                                                                                                                                                                                      PRT;
ö
                                              C.J., Infante D., Barbour Pof Borrelia hermsii linear
          HOST IMMUNE
ANOTHER
                                                                                                                                                                                                                                                     215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
.2e-09;
                                                                                                                                      Borrelia
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           RESPONSE
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CRC64;
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RESULT USO1_Y USO1_Y ID USO1_Y O1-MAY DT 01-MAY DT 02-MAY DT 02-MA
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Best Local S
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J. Cell
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.
USO1 OR INTI OR YDL058W.
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                                                                                                                                                                            Nakajima H., Hirata
Yamasaki M.;
                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1
                                                                                                                                                                                               MEDLINE-91185402; PubMed-2010462; Nakaima H., Hirata A., Ogawa Y.,
                                                                                                                                                                                                                                                                                                       Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P25386;
                           Kendrick K.E
                                             Hostetter M.
                                                                    SEQUENCE OF
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                        'A cytoskeleton-related gene, uso1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194
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                                                                                                             transport in Saccharomyces Biol. 113:245-260(1991).
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80; Conservative
    (FEB-1993)
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215 i
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                                             782-1790 FROM N., K., Herman D.J.,
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18 PROBABLE.
215 VARIABLE MAJOR C
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    EMBL/GenBank/DDBJ databases
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Pred.
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                                               Bendel
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                                             McClellan M.,
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CRC64;
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EMBL; L03188; AAB00143.1;
EMBL; U53668; AAB66659.1;
PIR; A38455; A38455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [3]
SEQUENCE OF 1-8 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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SGD; S0002216; USO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                     1159
                                                                                                                                           1039
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                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
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                                                                                                                 134
                                                                                                                                                                                                987
                                                              168
            211 LTEISKKITESNAVVLAVKEIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEE ER AND THE GOLGI COMPLEX.

BY AND THE GOLGI COMPLEX.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, CO OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.

SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: REQUIRED COMPLEX.
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                                                                                                                                           EEIISKSDSSKDEYESQISLLKEKLETATTANDENVNKISELTKTREELEAELAAYKNLK 1098
                                                                                                                                                                                                                    E------VETLLASIDELATKAIGKKIGNNGLEAN--QSKNTSLLSGAYAISDLTAEK 94
                                                                                                                                                                                                                                                 CNNLSKEKEHISKELVEYKSRFQSHDNLV--AKLTEKLKSLANNYKDMQAENESLIKAVE 986
                                                                                                                                                                                                                                                                            CNNSGKDG-----NASANSADESVKGPNLTEISKKI-----TESNAVVLAVK 44
                                   AQLKKYEEQIANKERQYNEEISQLN----DEITSTQQENESIKKKNDELEGEVKAMKSTS
                                                                                        NELETKLETSEKALKEVKENEEHLKEEKIQLEKEATETKQQLNSLRANLESLEKEHEDLA 1158
                                                                                                                                                                                              ESKNESSIQLSNLQNKIDSMSQEKENFQIERGSIEKNIEQLKKT-----ISDLEQTK 1038
                                                                                                               -----TDDNAQRAI------LKKHANKDKG-----AAELEKLFKAVENLS 167
                                                               -KAAQDTLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPN
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AA;
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                                                                                                                                                                                                                                                                                                                                                                 COLLED COLL (POTENTIAL).

CHARGED (HYPER-HYDROPHILIC).

CHARGED (HYPER-HYDROPHILIC).

DISPENSABLE FOR THE PROTEIN FUNCTION.

ASP/GLU-RICH (ACIDIC).

G -> E (IN REF. 2).

E -> K (IN REF. 2).

V -> I (IN REF. 2).

I -> V (IN REF. 2).

G -> S (IN REF. 2).

O -> DEEDDEE (IN REF. 2).

C -> CE2B216E9FD4818 CRC64;
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                                                                                                                                                                                                                                                                                                      Score 175; DB Pred. No. 0.51 66; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Golgi stack; Cytoskeleton; Coiled GLOBULAR HEAD.
            -TLLASIDELATKAIGKKIQQNGGLAVEAGH
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L BETWEEN THE
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                                                                                                                                                                                                                                                                                                                      Antigen;
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=99120557; PubMed=9923682;

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.

Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,

Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,

Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,

Tanno Taylor D.E., Voyis (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CAG PATHOGENICITY ISLAND PROTEIN 26).
CAGA OR CAI OR CAG26 OR JHP0495.
Helicobacter pylori J99 (Campylobacter pylori :
Bacteria; Proteobacteria; epsilon subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYTOTOXICITY ASSOCIATED IMMUNDDMINANT ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ZLT1;
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic sequence comparison of two unrelated isolates gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1320 TNLSK-----AKEKSESELSRLKKTSSEERKNAEEQLEKLKNEI 1358
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001483; AAD06073.1;
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                                                                                                                                                                                 NINKDLKDFSKSFDEFKNGKN-KDFSKAEETLKALKGSVKDLGINPEWISKVENLNAALN 751
                                                                                                                                                                                                              NSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKE------VETLLASID 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL 368
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NGTLYGNGLSKAEATTLSKNFSDIKKELNAKL--GNFNNNNNNGLENSTE----
                                                                                      ----CSTEFTNKLKSEHAVLGLDNLTDDN-AQRAILKKHANKDKGAAELEKLFKAVEN--
                                                                                                                                                  ELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQ-- 112
                                                                                                                                                                                                                                                105;
                                                         SVAKATGDFSG---VEQALADLKNFSKEQLAQQAQKNEDFNTGKNSA---
                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                       Complete proteome. 246 249
                   ----LSKAAQDTL----KNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTE 213
                                                                                                                                                                                                                                                                                                                          882
1167
                                                                                                                                                                                                                                                Conservative
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                                                                                                                       ----KNGKNKDFSKVTQ-----AKSDLENSIKDVIINQKITDKVDNLNQAV 795
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                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                        249 POLY-THR.
889 POLY-ASN.
; 129729 MW; FD5E86B81CEBD0F2
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                                                                                                                                                                                                                                                                Score 173.5;
Pred. No. 0.
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                                                             -LYQSVKNGV
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   -PIYTQ
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RRARRITA RANGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (Rel. 0
01-AUG-1988 (Rel. 0
20-AUG-2001 (Rel. 4
LAMININ BETA-1 CHAI
      Am. J. Hum. Genet. 41:605-615(1987).

Am. J. Hum. Genet. 41:605-615(1987).

IF FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

IS UBBURIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULEFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPAISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END. THE BETA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ), LAMININ-1 (MEROSIN), AND LAMININ-6 (K-LAMININ).

IN SUBCELLULAR LOCATION: EXTRACELLULAR.

IN SUBCELLULAR LOCATION: EXTRACELLULAR.

IN DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

IN SUMILARITY: CONTAINS 1 LAMININ NOMAIN DOMAIN (DOMAIN VI).

IN SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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P07942;
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Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1276-1709 FROM N.A. MEDLINE-88021029; PubMed-3661559; Jaye M., Modi W.S., Ricca G.A., M
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pikkarainen T., Eddy R., Fukushima Y., Byers M., Shows T., Pihlajaniemi T., Saraste M., Trygyvason K.; Pihlajaniemi T., Saraste M., Trygyvason K.; **Human laminin Bl Chain. A multidomain protein with gene (LAMB1) locus in the q22 region of chromosome 7.**; **J., Biol. Chem. 262:10454-10462(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vuolteenaho R., Chow L.T., Tryggvason K.;
"Structure of the human laminin B1 chain
J. Biol. Chem. 265:15611-15616(1990).
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ryota; Metazoa; (
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(LAMININ B1 CHAIN).
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EMBL; M61951; M58147; M55364; M55366; M55366; M55367; M55360; M55361; M55365; M55362 M55355 M55352 M5535 M55345 M55344 M55376 M61946 M61943; M61941; м61939; M61938 м61936; M61935 AAA59486.1; AAA59486.1; AAA59486.1; AAA59486.1; AAA59486.1; AAA59486.1; AAA59486 AAA59485 AAA59486. AAA59486. AAA59486. JOINED
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PRINTS; PROUD1; EGFLAMININ.
PRODOM; PROUD2082; LAMNT; 1.
SMART; SMO0136; EGF_LAM; 11.
SMART; SMO0136; EGF_LAM; 1.
SMART; SMO0136; LAMNT; 1.
PROSITE; PS00022; EGF_1; 9.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
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InterPro; IPR001886; LamNT.
InterPro: IPR002049; Laminin_EGF; I3
Pfam; PF00053; laminin_EGF; I3
Pfam; PF00055; laminin_Nterm;
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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MIM; 150240;
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S13547; N
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AAA59482.1;
AAA59487.1;
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n; Cell adhesion;
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DOMAIN ALPHA.

DOMAIN ALPHA.

DOMAIN I.

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RX MEDLINE-2019606; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Borkova D., Botchan M.R., Bouck J., Banddari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferracz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N. STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa, Arthropoda, Tracheata;
Pterygota; Neoptera; Endopterygota; Dipters
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DROME
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Query Match Best Local

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lilang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Relnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.*;
          CA_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caggese C., Ragone G., Perrini B., Moschetti R., de Caizzi R., Barsanti P.;
"Identification of nuclear genes encoding mitochondr isolation of a collection of D. melanogaster cDNAs h sequences in the Human Gene Index database.";
MOI. Gen. Genet. 261:64-70(1999).

-I- SUBCELTULAR ICCATION: MITOCHONDRIAL.
-I- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING D
-I- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN
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Pfam;
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Caggese C., Ragone G., Perrini B.,
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IPRO02024; Bacterioferritin.
IPRO03871; DUP223.
IPRO02048; EF-hand.
IPRO020861; REM_repeat.
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                8C710380263F262E CRC64;
                                   (POTENTIAL).
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(N REF. 2).
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ter cDNAs homologous to
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RESULT 9
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                       Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du g
A Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
A Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
A Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
A Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso I.
A Rifken L., Taich A., Trevaskis E., Vietation R.,
A Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.,
A Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.,
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
C. FOLE IN CROSSLINKING FILMENTS OF ANCHORING OTHER MOLECULE
C. ROLE IN CROSSLINKING FILMENTS OF ANCHORING OTHER MOLECULE
C. SUBCELLULAR LOCATION. NUCLEAR, TIGHTLY ASSOCIATED WITH THE
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01-OCT-1993 (Rel. 27, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN
NUF1 OR SPC110 OR YDR356W OR D9476.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mirzayan C., Copeland C.S., Snyder M.;
"The NUF1 gene encodes an essential coiled-coil related is a potential component of the yeast nucleoskeleton.";
J. Cell Biol. 116:1319-1332(1992).
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Eukaryota; Fungi; Ascomycota; Saccharomycetias; Saccharomycetales; Saccharomyces.
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"A spacer protein in the Saccharomyces cerevisiae spindle poly body whose transcript is cell cycle-regulated.";
J. Cell Biol. 123:1175-1184(1993).
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01-OCT-1993
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100; Conser
                                         -1998 (Rel. 36, Created)
-1998 (Rel. 36, Last sequence update)
-2001 (Rel. 40, Last annotation update)
(CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170).
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№; 04FAA074BB8A0BC8
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SEQUENCE FROM N.A.
MEDLINE-98137792; PubMed-9469933;
Griparic L., Volosky J.M., Keller T.C.
Griparic Chicken CLI
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DOMAIN
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Interpro; IPR001878; Znf_CCHC.
Interpro; IPR001878; Znf_CCHC.
Pfam; PF01302; CAP_GLY_I.
SMART; SM00343; Znf_C2HC; 1.
PR0SITE; PS00845; CAP_GLY_I.
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Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SEEMS TO BE A INTERNEDIATE FILAMENT ASSOCIATED PROTE:
-!- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE
--- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE
CYTOSKELETON (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS ARE PRODUCED BY
ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                         CONFLICT
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                  VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                561
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   127
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                                                                                                                     18 DESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKAIGKKIGNNGLEANQSKN 77
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VLGLDNLTDDNAQRAILKKHANKDKGA--AELEKLFKAVENLSKAAQDTLKN---
                               SSLKEKFESSEEALRKEIKTLSASNERMGKENESLKTKLDHANKENSDVIELWKSKLESA
                                                                                         DLALRVKEVAELRGRLESSK----HIDDVDTSLSLLQEIS--SLQEKMAAAGKE-HQREM 560
                                                                                                                                                   Similarity 22.936; Conservative
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458
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E -> V (IN REF. 2; A)
MW; 5631CE8683498E23
                                                                                                                                                 Score 158.5;
Pred. No. 2.2;
78; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coiled coil;
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CCHC-BOX.
MISSING (IN SHORT ISOFORM).
TOTKLEHARIKELEQSILFEKTKADKLORELEDTR ->
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S -> GGSSKVS (IN ISOFORM CLIP-170(11)).

T -> RKRQISEDPENT (IN ISOFORM CLIP-
                                                                                                                                                                                                                                                                     170(11+35))
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                                                           -KNEELKEKIDTAKQCSTEFTN--KLKSEHA 126
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CLIP-170
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498E23 CRC64;
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Best Local
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01-NOV-1997
                                                                                                                                                                                                        DOMAIN
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Tummuru M.K.R., Cover T.L., Blaser M.J.;
"Cloning and expression of a high-molecular-mass major antigen Helicobacter pylori: evidence of linkage to cytotoxin productio Infect. Immun. 61:1799-1809(1993).

-I- FUNCTION: MAY BE NECESSARY FOR THE TRANSCRIPTION, FOLDING,
                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                          EMBL; L11714; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                   entitles requires a license agreement (See http://www.isb-sib.
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision;
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                                                                                                                                                                                                                                Antigen.
                                                                                                                                                                                                                                              HSSP; P02937; 1MLP.
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                                                                                                                                                        Local Similarity
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 LGLDNLTDDNAQR----AILKKHANKD-----
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                                                                                       PNLNNLAITSVVRRDLEDKLIAKGLSPQEANKLVKDFLSSNKELVGKAL----NFNKAV
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1182 AA;
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                                       -GNYDEVKRAQKDL--
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35, Last sequence update)
35, Last annotation update)
CIATED IMMUNODOMINANT ANTIGEN
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Pred. No. 1.
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                                       EK - - SLKKREHLEKGDVAKNLESKSGNKNKMEAK -
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01-AUG-1988
01-AUG-1988
20-AUG-2001
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-86111835; PubMed-3511046; MEDLINE-86311835; PubMed-3511046; MEDLINE-86311835; PubMed-3511046; MEDLINE-MARKET V.F.,
                                                                                                                                                                                                                                                                                                                                          Scott J.R., Pulliam W.M., Hollingshead S.K., Fischetti V.A.; "Relationship of M protein genes in group A streptococci."; "Relationship of M protein genes in group A streptococci."; "Rolationship of M protein U.S.A. 82:1822-1826(1985).
-i- FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SERCOF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VINULENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hollingshead S.K., Fischetti V.F., Scott
"Complete nucleotide sequence of type 6
Streptococcus. Repetitive Structure and
                Pfam; PF00746; Gram_pos_anchor;
Pfam; PF02370; M; 9.
                                           PIR; A26297; A26297.
InterPro; IPR001899; Gram_pos_anchor
InterPro; IPR003345; M_repeat.
                                                                                                                                      entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus.
J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M6_STRPY
                                                                                         EMBL; M11338;
                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 43-122 FROM N.A. MEDLINE=85166224; PubMed=3885219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
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SIMILARITY: TO OTHER M PROTEINS.
SIMILARITY: TO OTHER STREPTOCOCAL AND
IN THE REGION OF THE MEMBRANE ANCHOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 08, Created)
(Rel. 08, Last sequence update)
(Rel. 40, Last annotation updat)
SEROTYPE 6 PRECURSOR.
                                                                                           AAA26920.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261:1677-1686(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                      license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scott J.R.;
                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483
                                                                                                                                        (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M protein of the membrane anchor.'
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                                                                                                                                                                                                                                                                STAPHYLOCOCCAL
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                                                                                                                                                                                                                                                                                                                                RESISTANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group
                                                                                                                                                                                                                                                                  PROTEINS
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                                                                                                                                                                                                                                                                                                                                               엱
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RBP2_PLAVB
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Matches 109
                                                                                                              01-APR-1993
01-APR-1993
01-OCT-1996
SEQUENCE FROM N.A.
MEDLINE-9315338; PubMed-1617731;
Galinski M.R., Medina C.C., Ingra-
"A reticulocyte-binding protein co
                                                                                                                                               RBP2_PLAVB
Q00799;
                                                                   Eukaryota;
                                                                            Plasmodium vivax (strain
                                                        NCBI_TaxID=31273;
                                                                                                    RETICULOCYTE
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                            AVENLAKAAKEMLANSVKEL
                                                                                                                                                                                                                                                                                                                        DELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKL--ITQKLDGLKNSEK-----
                                                                                                                                                                                                                AE---AKALKEQLAKQAEEL
                                                                                                                                                                                                                                                          GLRRDLDASREAKKQVEKALEEANSKLAALEKLNKELEESKKLTEKEK---
                                                                                                                                                                                                                                                                                                     QELAKKDEGNKVSEASRKGLRRDLDASREAKKQVEKDLANLTAELDKVKEEKQISDASRQ
                                                                                                                                                                                                                                                                                                                                                                                                                   AELEKLFK-AVENLSKAAQDTLKNAV-KELTS--
                                                                                                                                                                                                                                                                                                                                                                       GNTSANSADESVKGPNLTEISKKITESNAVVLAVKEI--ETLLASI-------
                                                                                                                                                                                                                                                                               - LKEKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFK
                                                                                                                                                                                                                                                                                                                                                IGTLKKTLDETVK----DKIAKE-QESKETIGTLKKILDETVKDKIAREQKSKQDIGALK
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DQNKNLTTENKNLTDQNKNLTTE-NKELKAEE-----NRLTTEN--KGLTKKLSEAEEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KN--EELKEKIDTAKQCSTEFTNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNKYDVENSMLQANNDKLTTE-----NNNL-TDQNKN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAVKEVET - - LLASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAKNNTNRHYSLRKLKKGTASVAVA-LSVIGAGLVVNTNEVSARVFPRGTVENPDKAREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                   Alveolata;
                                                                                                             (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                    BINDING
                                                                                                                                                          STANDARD;
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                                                                                                           25, Created)25, Last sequence update)34, Last annotation updat
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448
454
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487
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269
347
                                                                                                 PROTEIN 2 (FRAGMENT).
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24.8%;
                                                                  Apicomplexa;
.C., Ingravallo P., protein complex of
                                                                             Belem)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 157.5; D
Pred. No. 0.75;
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GLY/PRO-RICH (CELL WALL-SPANNING)

CONSERVED IN GRAM-POSITIVE COCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 x 7 AA TANDEM REPEATS.
4.5 x 25 AA TANDEM REPEATS.
TWO DIRECTLY REPEATED 27 AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M PROTEIN, SEROTYPE 6.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEINS
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                                                                                                                                                          PRT;
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                                                                Haemosporida;
                                                                                                                                                          1251
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                                                                                                            update)
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Barnwell J
Plasmodium
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                                                                Plasmodium
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J.W.;
um vivax
                                                                                                                                                                                                                                                                                                                                                                                                                   -- PIVHGNNSGKD
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                                                                                                                                                                                                                                                           -AELQAKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113;
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                                                                                                                                                                                                                                                                                                                                                                                                                   194
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                              MST2_DROHY
Q08696;
                                                                                                                   01-FEB-1995
01-FEB-1995
20-AUG-2001
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musci
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7224;
                                                              MST101(2).
Drosophila hydei (Fruit fly)
                                                                                                                                                                                                                                                    1054
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NON_TER
SEQUENCE
                                                                                                   AXONEME-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            merozoites.";
Cell 69:1213-1226(1992).
-i- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY
HUMAN RETICULOCYTE CELLS.
-i- SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entitles requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M88098; AAA29744.1; -.
                                                                                                                                                                                                                                                                                                           998
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                                                                                                                                                                                                                                                                               TDA - - - - AKDKG - - - - -
                                                                                                                                                                                                                                               TDSKTIISKLKGVIIEVNENTEMNTIESSAKEIEALYNELKNKKTSLNEIYQTSNEVK
                                                                                                                                                                                                                                                                                                        EKNVKAYLAYIK--KNYEDTVQDVLTLNEHFNTKQVSNHEPTNFDKSNKSSEELTKA--V
                                                                                                                                                                                                                                                                                                                                     SKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQLGIE--NVTDENAKKAILI
                                                                                                                                                                                                                                                                                                                                                                 ETDIDSLNTALDELLKKGRTCEVSRYKLIKDTVTKEISDDTEL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLFKAVENLSKAAQDTLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EHAVLG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVALEILAH----SDEIDTKQKDSSKLIEMGNQIYLKVVLINQYKNKISSIKSKEEAVSVK 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEKLNVLKNEELKEKIDTAKQCST-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGNASANSADESVK----GPNLTEISKKITESNAVVLAV-----KEVETLLASIDELAT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGNVSKKHSELSKITCSDKSYDNIIALEKQTELQNLRNSFTQE---KTNTNSD---SKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor; Membrane.
                                                                                 (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
(OCIATED PROTEIN MST101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \frac{1251}{1251}
                                                                                                                                                                                                                                                                                                                                                                                                                         ----KTDFESLKNALKTLEGE-VNALKASSDNHEHVQSKSEPV-NPALSEIEKE
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                                                                                                                                                                           STANDARD;
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A; 143741 MW;
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21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 157.5;
                                                                                                                                                                                                                                                                            ----AAELEKLFKAVENLAKAAKEM--LANSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54BA51C7404AC572 CRC64;
                                                                                                                                                                           1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LDNLTDDNAQRAILKKHANKDKGAAELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----EFTNKLKS-----
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                                                                                                                                                                          A
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                                          Muscomorpha;
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RESULT 15
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Eur. J. Biochem. 225:1089-1095(1994).
Eur. FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE
-I- SUBCELLULAR LOCATION: CYTOPLASMIC.
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MYSN_DROME Q99323;
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POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE
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                                                                                          AAKKEKEAAEREKCGELAKKIKKAAEKKKCKKLAKKEKE
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Repeat; Multigene family; Polymorphism.

32 1268 59 x 16 AA APPROXIMATE TANDEM REPEATS

[KR]-K-X-C-X-X-X-K-X-X-K-X-X-X-X-E.

4 391 AA; 159000 MW; 1B2A368F30F48878 CRC64;
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an email to license@isb-sib.ch).
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                STANDARD;
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Pred. No. 2.
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MYOSIN HEAVY (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ketchum A.S., Stewart C.T., Stewart M., Kiehart D.P.;

"Complete sequence of the Drosophila nonmuscle myosin heavy-chait
transcript: conserved sequences in the myosin tail and different
splicing in the 5' untranslated sequence.";

Proc. Natl. Acad. Sci. U.S.A. 87:6316-6320(1990).

-1- FUNCTION: NONMUSCLE MYOSIN APPEARS TO BE RESPONSIBLE FOR
-1- FUNCTION: REQUIRED FOR MORPHOGENESIS AND CYTOKINESIS.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) A
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
SEQUENCE
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Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEANY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000048; IQ.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
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B36014; B36014.
  LTEISKKITESNAVV---
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation updat
Y CHAIN, NON-MUSCLE (ZIPPER PROT
                                                                   Conservative
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LAVKEVE---TLLASIDELATKAIGKKIG---
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MISSING (IN SHORT ISC
MW; 73E3CB02BABF2528
                                                              Score 155.5;
Pred. No. 4.3;
55; Mismatches
                                                                                                                                                                                                                                    LIGHT MEROMYOSIN (LMM).
ALPHA-HELICAL TAILPIECE (LMM).
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50 KDA/20 KDA JUNCTION.
ACTIN-BINDING.
REACTIVE SULFHYDRYL/ACTIN-BINDING
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tail and differential
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122 TL------KRSLEBETVNHEGVLADMRHKHSQELNSINDQLENLFKAKTVLEKAKG 1271
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                                                                                                                                             1327 TKLQQEAENITNQL-EEAELKASAAVKSASNMESQLTEAQQLLEEETRQKL-GLSSKLRQ 1384
                                                                                               287 ----SEKLKEKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAE 342
                                                                                                                                                                              233 TLLASIDELATKAIGKKIQQNGGLAVEAGHN--GTLLAGAYTISKLITQKLDGLKN---- 286
                                                                                                                                                                                                                                              173 TLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIE 232
                             343 LE----KLFKAVENLAKAAKEMLANS 364
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Search completed: March 18, 2002, 10:11:57 Job time: 975 sec

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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 11, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
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EMBL; U04240; AAC45538.1;

InterPro; IPRO1800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

SEQUENCE 209 AA; 22393 MW; 3707A47DAA736FCA CRC64;
                                                                                                           SEQUENCE FROM N.A.
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       Gibbs C.P.,
for lateral
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G (TrEMBLrel.
L (TrEMBLrel.
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ilarity 98.9%;
Conservative
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Spirochaetaceae; Bor
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, Last sequence up
, Last annotation
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Pred. No. 3.1e-35;
2; Mismatches 0;
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             recombination
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Best Local
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O31117;
O1-JAN-1998
O1-JAN-1998
O1-JUN-2001
                                                                                                                                                                                                                                              NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                    Wang I.-N., Dykhuizen D.E., Dunn J.J., Luft B. Submitted (OCT-1997) to the EMBL/GenBank/DDBJ EMBL; AF029866; AAB86549.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=OC7;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OUTER SURFACE
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyme disease Borrelia.";
Mol. Microbiol. 18:257-269(1995).
EMBL; L42894; AAB37002.1; -.
                                                                                                                             3 CNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKAIG
           LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE
                                                                      IGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNYLKNEELKEKIDTAKQCSTEFTNK 120
                                                                                                                ISCNNSRKDGNASTNSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKA
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LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE
                                                       IGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNK 126
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                                                                                                                                                                         182;
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                                                                                                                                                                                                                                                                                     FU1441; Lipoprotein_6; 1. PD001149; Lipoprotein_6; 1.
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192 AA;
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                                                                                                                                                                       49.48; ilarity 97.88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
CE PROTEIN C (FRAGMENT).
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                                                                                                                                                                                                                                         192
; 20684 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                disease spirochete).
Spirochaetaceae; Borrelia.
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; Pred. No. 3.5e-35;
; Pred. No. 3.5e-35;
                                                                                                                                                                       Pred. No. 1e-: 2; Mismatches
                                                                                                                                                                                Score 889; Db 2,
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                                                                                                                                                                                                  DB 2;
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databases.
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                                                                                                                                                                                                                                              CRC64;
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Best Local Similarity
Matches 180; Conserv
STRAIN-OC12:
Wang I.-N. Dykhuizen D.E., Dunn J.J.,
Wang I.-N. Dykhuizen D.E., Dunn J.J.,
Submitted (OCT-1997) to the EMBL/GenBe
EMBL; AF029871; AAB86554.1; -.
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                         O31122
PKELLING
O31122;
O31122;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
O1-JUN-2001 (TREMBLREL C (FRAGMENT).
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updato)
01-SURFACE PROTEIN C (FRAGMENT).
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InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
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Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi (Lym. Bacteria; Spirochaetales; NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Mol. Microbiol. 18:257-269(1995).
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01-MAY-2000 (TrEMBLrel.
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pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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O31123;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence up
O1-JUN-2001 (TrEMBLrel. 17, Last annotation
OUTER SURFACE PROTEIN C (FRAGMENT).
                                                                                                         SEQUENCE
                                                                                                                                          Wang I.-N., Dykhuizen D.E., Dunn J.
Submitted (OCT-1997) to the EMBL/Gei
EMBL; AF029872; AAB86555.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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Bacteria; Spirochaetales; Spirochaetaceae;
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SEQUENCE
189 NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETTLLASIDELATKAIGK 248
                                                                                                                                                                                                                       STRAIN=OC13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fung B.P., McHugh G.L., Leong J.M., Steere A.C.;
"Humoral immune response to outer surface protein C of Borrelia burgdorferi in Lyme disease: role of the immunoglobulin M response the serodiagnosis of early infection.";
Infect. Immun. 62:3213-3221(1994).
EMBL; U08284; AAA21460.1;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence updat
01-JUN-2001 (TrEMBLrel. 17, Last annotation upd
OUTER SURFACE PROTEIN C (FRAGMENT)
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borr
                                                                                                                                 NON_TER
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Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            NCBI_TaxID=139;
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185 AA;
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                                         Conservative
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19673 MW;
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                                                   46.8%;
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                                       Score 841; DE
Pred. No. 1.6e
2; Mismatches
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Last annotation updat
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Pred. No. 1.6e-33;
D; Mismatches 1
                                                                                                     58D6FEE3C7769CAF CRC64;
                                                                                                                                                                                                          J.J.,
                                                                                                                                                                                                                                                                                   spirochete)
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1.6e-32;
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Best Local Sin
Matches 171;
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Q44979;
01-NOV-1996
                                                                                Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; ; NCBI_TaxID=139;
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01-JUN-2001
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
OUTER SURFACE PROTEIN C (FRAGMENT).
                                          SEQUENCE FROM N.A.
                                                                                                                                                                        OUTER SURFACE
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EMBL; X84779; CAA59250.1; -.

Interpro; IPR001800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6; 1.
  MEDLINE=95286481;
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Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; S
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Theisen M., Borre
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(TIEMBLIEL 01, Last sequence
(TIEMBLIEL 17, Last annotatic
E PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Matches 170; Conserv
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EMBL; X84782; CAA59253.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_5; 1.
ProDem; PD001149; Lipoprotein_6; 1.
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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178 /
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nilarity 98.3%;
Conservative
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; 18818 MW;
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M., Mathiesen M.J.,
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Pred. No. 1.1e-31;
1; Mismatches 2;
                                                                                                                                                                                                                                   Score 739; DB 2;
Pred. No. 8.4e-28;
5; Mismatches 13
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Best Local S
Matches 139
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031115;
01-JAN-1998
01-JAN-1998
01-JUN-2001
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Q44705;
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EMBL; U01892; AAA16057.1; -.
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
SEQUENCE 212 AA; 22270 MW; FB2E
                     Wang I. N., Dykhuizen D.E., Dunn J.
Submitted (OCT-1997) to the EMBL/Ge
EMBL, AF029862; AAB86545.1; -.
InterPro; IPR001800; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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                                                                                                                                                                                                           Bacteria; Spiro
NCBI_TaxID=139;
                                                                                                                                                                                                                                                      Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                                                                                             OUTER SURFACE
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"Molecular characterization and expression
American strain of Borrelia burgdorferi.";
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                                                                                                                                                                        SEQUENCE FROM N.A.
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ACE PROTEIN C
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  Lipoprotein_6; 1.
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72.4%;
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spirochaetaceae;
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Last annotation updat
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Last sequence up
                                                                                                       Dunn J.J., Luft B. EMBL/GenBank/DDBJ
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Pred. No. 9.5e
21; Mismatches
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pression of p23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ery Match 35.9%;
Sest Local Similarity 70.7%;
Matches 133; Conservative 2
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SEQUENCE
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"B. tanuki(Strain Fi8lt) ospC, partial cds.";
"Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000354; BAA19087.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD00149; Lipoprotein_6; 1.
NON_TER 1 1
NON_TER 202 202
SEQUENCE 202 AA; 21536 MW; F309F684C68961E7 CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
0UTER SURFACE PROTEIN C (FRAGMENT).
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=56146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-FI81T;
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  191 KELTSPVV 198
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20596 MW; 018A4CB310475A58 CRC64;
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B.burgdorferi stra	1 anti	garinii OspC.	Borrelia JSB antig	B. burgdorferi str	B afzelii ospC pro	B. afzelii OspC.	feri	B garinii ospC pro	B burgdorferi ospC	B31 outer surface	B burgdorfer1 ospC	B31 Osp-A/antigen	Borrelia IP2 OspC		Outer surface prot	urgdorferi	B31 outer surface	ia sp	ia sp	qs		co	lia sp	ia sp chime	ia sp chime	lia s	lia sp	lia sp	-		Ö	relia sp c	Borrelia sp chimer

ALIGNMENTS

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03-APR-2001 (first entry)

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XX AAA Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses Chimeric -Chimeric -WPI; 2001-050113/06. N-PSDB; AAF29028. Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick Borrelia sp chimeric ospC protein SEQ ID to Lyme disease Dattwyler RJ, (UYNY) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC. 18-JUN-1999; 19-JUN-2000; 2000WO-US16915 28-DEC-2000 WO200078966-A1 Borrelia sp. Borrelia sp. Seinost G, 9905-0140042 Dykhuizen D, Luft ŏ. 52 밍 Gomes-Solecki

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Best Local Similarity
Matches 364; Conserv
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DB; AAF29031.
       standard;
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Pred. No. 3e-109;
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Lyme disease are used
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                                                 AKAKKCSEEFTNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLL
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disease.
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Pred. No. 1.3e-107;
1; Mismatches 3;
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Lyme disease are used
to Lyme disease -
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Chimeric -
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Borrelia sp.
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66.7%;
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                                                                                                     Score 1726.5; DB 22
Pred. No. 2.2e-107;
2; Mismatches 3;
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Chimeric -
                                  Claim 43;
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                                  Page 81; 160pp;
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Borrelia
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                                                                                                                                  99US-0140042
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The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads

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Query Match Best Local

Matches

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Mismatches

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Score 1491.5; Pred. No. 9.3

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DB 22; 43;

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                                     WPI; 2001-050113/06
N-PSDB; AAF29033.
                                                           Dattwyler RJ,
                                                                                                18-JUN-1999;
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                                                                                                                                              WO200078966-A1
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             from strains of Borrelia which cause animals and detect immune responses
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Matches 308; Conser
WPI; 2001-050113/06
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                                                                                                                                                                                                                                                                                                                                                           Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia sp chimeric ospC protein SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia; ospC; Lyme disease;
                                                                                            (UYNY ) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC.
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to Lyme disease -
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tive 23; Mismatches 43
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Chimeric -
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be used as
lcks and leads
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                                                  The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as
                          vaccines against Borrelia infection, to Lyme disease.
                                                                                                                              Sequence
                                                                                                      Claim 43; Page 136-137; 160pp;
                                                                                                                                                                                  WPI; 2001-050113/06.
N-PSDB; AAF29037.
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Search completed: March 18, 2002, 09:54:35 Job time: 333 sec

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ALIGNMENTS

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US-09-596-746-52
US-09-596-746-52
Sequence 52, Application US/09596746
SERERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
FILE REFERENCE: 2631.1002-001
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                                                                                                                                                                             ; TYPE: PRT; ORGANISM: OSPC Chimera US-09-596-746-52
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                                                                                                                                                                                                                                    SOFTWARE: F
SEQ ID NO 52
LENGTH: 560
                                                                             Query Match
Best Local Similarity
Matches 560; Conserv
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
FastSEQ
                                                                             Conservative
                                                                                                                                                                                                                                                                             for Windows Version 4.0
                                                                                               100.0%; Score 2750; DB 19; 100.0%; Pred. No. 1.1e-180;
                                                                               0;
                                                                               Mismatches
                                                                                 Indels
                                                                                                                    Length 560;
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                                                                               0;
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                                                                                                                                           ; TYPE: PRT
; ORGANISM: ospC Chimera
US-09-596-746A-52
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LENGTH: 560
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Best Local
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                                                                                                                                                                                                   ITLE OF INVENTION: Groups of Borrelia burgdorferi and TTLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
COPTUANDE: FESTER FOR WINDOWS VARRENT A N
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                        61
                                                                                  / Match 100.0%; Score 2750; DB 19; Local Similarity 100.0%; Pred. No. 1.1e-180; nes 560; Conservative 0; Mismatches 0;
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Luft, Benjamin J.
Maria J.C. Gomes-Solecki
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Seinost, Gerald
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITILE OF INVENTION: Groups of Borrelia burgdorferi and
TITILE OF INVENTION: Borrelia afzelii That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTMARE: FastSEQ for Windows Version 4.0
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; GENERAL INFORMATION:
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TYPE: PRT
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SEEFTNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVA 367
                                         LAKKAIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKC 307
                                                                                LAKKAIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKC
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                                                                                                                                                       63.9%;
95.1%;
                                                                                                                                                    Score 1758; DB 19;
Pred. No. 1.6e-112;
                                                                                                                                         Mismatches
                                                                                                                                                                    DB 19;
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                                                                                                                                                                   Length 410;
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US-09-596-746A-84
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Best Local Sim
Matches 366;
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SEQ ID NO 84
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SED ID NOS: 84
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TYPE: PRT
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                                                                                                                                                                                                                                                                                               Local Similarity
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                                            VKEVEALLSSIDELSKAIGKKIKNDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEE
                                                                                          LTNSVKELGH------RNNSGGDSASTNPDESAKGPNLTVISKKITDSNAFLLA 415
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LKKKIKEAKDCSQKFTTKLKDSHAELGIQSVQDDNAKKAILKTHGTKDKGAKELEELFKS
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                                                                                                                                                                                                                                                                                     Conservative
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95.18;
                                                                                                                                                                                                                                                                                   Score 1758; DB 19;
Pred. No. 1.6e-112;
0; Mismatches 7;
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US-09-596-746A-58

Sequence 58, Application US/09596746A
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia
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US-09-596-746-58
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SOFTWARE: FastSEQ for
SEQ ID NO 58
LENGTH: 386
TYPE: PRT
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Best Local Similarity
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APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
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95.8%;
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Luft, Benjamin J.
Maria J.C. Gomes-Solecki
WENTION: Groups of Borre

Borrelia

burgdorferi

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FILE REFERENCE: 2631.1002-UU1
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 385
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; TYPE: PRT
; ORGANISM: OSPC C
US-09-596-746A-58
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Sequence 56, Application US/09596746A
GENERAL INFORMATION:
LENGTH: 385
TYPE: PRT
ORGANISM: OSPC Chimera
-09-596-746A-56
                                                                                                                                                                 APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D:
FILE REFERENCE: 2631.1002-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.8%;
Best Local Similarity 95.8%;
Matches 364; Conservative
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SEQ ID NO 58
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CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEO ID NOS: 84
CORMINADE: SEO ID NOS: 84
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Pred. No. 2.8e-112;
0; Mismatches 4;
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Query Match
Best Local Similarity
Matches 374; Conserv

Conservative

62.9%;

Score 1729.5; Pred. No. 1.3e 1; Mismatches

1.3e-110; hes 3;

181;

Gaps

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DB 19; Length 384;

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; TYPE: PRT; ORGANISM: OSPC Chimera US-09-596-746-56
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US-09-596-746-56
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SEQ ID NO 56
LENGTH: 384
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                                                                PRIOR APPLICATION NUMBER: US 60/140,04
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                  APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
                                                                                                                          CURRENT APPLICATION NUMBER: US/09/596,746 CURRENT FILING DATE: 2000-06-16
                                                                                                                                                 TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D FILE REFERENCE: 2631.1002-001
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Best Local Similarity
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                                                                                                      2000-06-16
3ER: US 60/140,042
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67.0%;
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Pred. No. 6.1
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APPLICANT: Luft, Benjamin J.

APPLICANT: Maria J.C. Gomes-Solecki
FITTLE OF INVENTION: Groups of Borrelia burgdorferi and
FITTLE OF INVENTION: Borrelia afzeili That Cause Lyme Disease in Hume
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT EILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 78
LENGTH: 408
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; Sequence 78, Application US/09596746
; GENERAL INFORMATION:
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                                                         Query Match
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APPLICANT:
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2 ACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAAQVALTNSVKELGHRNNSGGDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEA 421
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                                             373; Conserv
                                                                                                                                                                                                                                                                                                                                             Seinost, Gerald
Dykhuizen, Danial
                                                                                                                                                                                                                                                                                                                                                                         Dattwyler,
                                             Conservative
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                                                        62.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                           Raymond J.
                                          Score 1726.5; DB 19
Pred. No. 2.4e-110;
2; Mismatches 3;
                                                                      DB 19; Length 408
                                             Indels
                                            181;
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                                          Gaps
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                                                                                                                                                                US-09-596-746A-78
                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-6-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 78
                                                                                    Query Match 62.8
Best Local Similarity 66.7
Matches 373; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 78, Application US/09596746A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631 1002-001
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/596,746A CURRENT FILING DATE: 2000-06-19
                                                                                                                                                                                            LENGTH: 409
TYPE: PRT
                                                                                                                                                                              ORGANISM: ospC Chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384
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                           EAKDCSQKFTTKLKDSHAELGIQSVQDDNAKKAILKTHGTKDKGAKELEELFKSLESLSK
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 GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK 121
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                                                                                                                                                                                                                                         for Windows Version 4.0
                                                                                                    62.8%;
66.7%;
                                                                                      Score 1726.5; DB 19
Pred. No. 2.4e-110;
2; Mismatches 3;
                                                                                                                      DB 19;
                                                                                       Indels 181;
                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                              Disease in Humans
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APPLICANT: Dattwyle
APPLICANT: Seinost,
APPLICANT: Dykhuize
APPLICANT: Luft, Be
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SOFTWARE: FAS
SEQ ID NO 26
FNGTH: 374
                                                                                                                               Query Match
Best Local Similarity
                                                                                                                     Matches
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4.
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease ILE REFERIOE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION SUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                 TYPE: PRT
                                 61
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                                                       MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
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||||||||||||||||||||||||||
AAQAALTNSVKELTNPVVA 403
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                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                               Luft, Benjamin J.
Maria J.C. Gomes-Solecki
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                                                                                                                    Conservative
                                                                                                               54.4%; Score 1496.5; DB
82.7%; Pred. No. 1.5e-94;
tive 21; Mismatches 43
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                                                                                                                                             DB 19;
                                                                                                                  43;
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SEQ ID NO 24
LENGTH: 375
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
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                LVLSIDELAKKAIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTE 300
                                                                                  ELTSPVVAESPAMGSNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVET 240
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LLTSIDELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAE
                                                                                                                                      KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                   ELTSPVVAESPAMVNNSGKDGNT-SANSADESVKGPNLTEISKKITESNAVVLAVKEVET
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Maria J.C. Gomes-Solecki
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Seinost, Gerald
Dykhuizen, Danial
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                                                                                                                                                                                                                                                                                                                                            54.3%; Score 1492; DB 19; 83.5%; Pred. No. 3e-94; tive 20; Mismatches 40;
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 373
TYPE: PRT
RESULT 14
US-09-596-746-62
; Sequence 62, Application US/09596746
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US-09-596-746-26
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GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Scinost, Gerald
APPLICANT: Scinost, Gerald
APPLICANT: Dykhuizen, Danial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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CURRENT ADDITIONTON
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                                                                                           KAAKEMLANSVKEL 373
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FILE REFERENCE: 2631.102-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION UMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 62
LENGTH: 397
TYPE: PAT
ORGANISM: OSPC Chimera
US-09-596-746-62
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                                                                                                                                                                                                                : Sequence 62, Application US/09596746A
; GENERAL INFORMATION:
; APPLICANT: Dattwyler, Raymond J.; APPLICANT: Seinost, Gerald
; APPLICANT: Dykhuizen, Danial
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APPLICANT: Seinost, Gerald
APPLICANT: Dykhulzen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
                                                   TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
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                                   PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-
                    NUMBER OF SEQ ID NOS:
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Maria J.C. Gomes-Solecki
FastSEQ for Windows Version 4.0
                                     1999-06-18
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                                                                                                                                                                                                                              ; SEQ ID NO 62
; LENGTH: 398
; TYPE: PRT
; ORGANISM: OSPC Chimera
US-09-596-746A-62
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                                                                                                                                                                                          Query Match 54.1%; Score 1488.5; DB 19; Length 398; Best Local Similarity 82.4%; Pred. No. 5.8e-94; Matches 308; Conservative 22; Mismatches 43; Indels 1;
362 KAAQVALTNSVKEL 375
|||: | ||||||
385 KAAKEMLANSVKEL 398
                        1; Gaps
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Search completed: March 18, 2002, 10:08:47 Job time: 975 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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       d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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2750
1 MACNNSGKDGNTSAN
       March 18, 2002, 09:55:35; Search time 55.5 Seconds (without alignments) 227.060 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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       DB
  US-08-235-836C-110
US-08-235-836C-20
US-09-158-35-3
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US-08-235-836C-107
US-08-235-836C-34
US-08-235-836C-34
US-08-235-836C-34
US-08-235-836C-36
US-09-196-293-11
US-08-158-35-2
US-08-158-35-3
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Compugen Ltd.
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Sequence 110, App Sequence 15, Appli Sequence 15, Appli Sequence 112, Appli Sequence 117, Appli Sequence 117, Appli Sequence 34, Appli Sequence 36, Appli Sequence 31, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli
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                                                  Query Match 35.9%; Score 986.5; DB 4; Best Local Similarity 51.1%; Pred. No. 8e-63; Matches 256; Conservative 42; Mismatches 132;
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US-08-235-836C-110 US-08-235-836C-110 US-08-235-836C-110 Sequence 110, Application US/08235836C Patent No. 6248562 GENERAL INFORMATION: APPLICANT: Dunn, John J. APPLICANT: Dunn, John J. APPLICANT: Luft, Benjamin J. APPLICANT: Dunn, John J. APPLICANT: Luft, Benjamin J. APPLICANT: Lutt, Benjamin J. APPLICANT: Lutt, Benzelia Polypeptides and Uses There CORRESPONDENCE ADDRESS: 144 CORRESPONDENCE ADDRESS: 144 CORRESPONDENCE ADDRESS: ADDRESSEE: Brookhaven National Laboratory STATE: NY COUNTRY: USA ZIP: 11973 COMPUTER READABLE FORM: MEDDUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDDUM TYPE: Floppy disk COMPUTER READABLE FORM: COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/235,836C FILING DATE: 29-APR-1994 CLASSIFICATION NUMBER: US/08/235,836C FILING DATE: 01-11-93 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: US/08/235,836C FILING DATE: 01-11-93 ATTORNEY/AGENT INFORMATION: NAME: Bogosian, Margaret C. REGISTRATION NUMBER: US/08/235,836C FILING DATE: 01-11-93 ATTORNEY/AGENT INFORMATION: TELEPHONE: (516) 282-7329 INFORMATION FOR SEQ ID NO: 110: SEQUENCE CHARACTERISTICS: LENGTH: 466 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: protein US-08-235-836C-110	28 177.5 6.5 1196 2 US-08-735-893-4 29 177 6.4 1388 2 US-08-685-576-1 30 176.5 6.4 3248 1 US-08-353-700-1 31 176.5 6.4 3248 5 PCT-US95-16216-1 32 175.5 6.4 2482 1 US-08-328-254-6 33 174 6.3 1038 4 US-08-328-254-6 35 171 6.2 1104 4 US-08-923-992A-4 35 171 6.2 1104 4 US-08-923-992A-4 36 170.5 6.2 1151 3 US-08-840-006-5 38 170.5 6.2 1151 3 US-08-840-006-5 38 170.5 6.2 1151 3 US-08-840-006-5 40 170.5 6.2 3111 2 US-08-840-006-5 41 167 6.1 1147 3 US-08-125-077-4 42 167 6.1 1147 3 US-08-125-077-4 43 167 6.1 1147 3 US-08-470-260-5 44 167 6.1 1147 3 US-08-470-260-5 58 167 6.1 1147 4 US-08-195-487-4 59 167 6.1 2101 5 PCT-US93-06160-4 50 SIGNMENTS
Comprising	Sequence 1 Sequence 1 Sequence 1 Sequence 6 Sequence 4 Sequence 4 Sequence 6 Sequence 6 Sequence 6 Sequence 6 Sequence 7 Sequence 8 Sequence 8 Sequence 9 Sequence 9 Sequence 4 Sequence 4 Sequence 5
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1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60

Length Indels

466; 71;

Gaps

17;

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Gaps

0,

196

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RESULT 2
US-08-235-836C-30
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: No. 6248562el Chimeric Proteins Comprising
APPLICANT: No. 6248562el Chimeric Proteins Comprising
APPLICANT: No. 6248562el Chimeric Proteins Comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30, Application US/08235836C Patent No. 6248562
                           NFORMATION FOR SEQ ID NO:
                                                                               NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BL193-28A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: No. 6248004621 CHARLOS TITLE OF INVENTION: Borrelia Polypeptides and Uses WIMMER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Brookhaven National Laboratory
                                                            TELEPHONE:
                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 29-APPLICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Upton
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 GKTLVSKKVTSKDKSSTEEKFNEKGEVSEKIITRADGTR-----LEYTGIKSDGSGKA
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 11973
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                                                              (516) 282-7338
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                                                                                                                                                                                                                                                                                                                       Version #1.25
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APPLICANT: Soutscheck, Erwin
APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Preac Mursic, Vora
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.001US2
CURRENT APPLICATION NUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER FILING DATE: 1994-03-10
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1992-06-19
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
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; ORGANISM: Borrelia burgdorferi
US-09-196-293-15
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                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 15
LENGTH: 209
                                                                                                                                                     Matches
                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                        LENGTH: 20
TYPE: PRT
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Best Local
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MOLECULE TYPE:
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                  61 IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN
                                                                      17
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 33.9%;
Local Similarity 98.4%;
                                                            188;
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                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            NUMBER: DE P40 18 988.0
33.7%;
                                                                                                                                                                  Score 928; DB 4
Pred. No. 4e-59;
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Pred. No. 2.1e-59;
                                                                                                                                               Mismatches
                                                                                                                                                                                  DB 4; Length 209
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Best Local Similarity
Matches 188; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -08-158-353-3
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
                                                                                                                                                                                                                                                                                           08-158-353-3
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                        TOPOLOGY: 15
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137
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                                                                    121 KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
 197
                           181 ELTSPVVAESP 191
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                                                                                                                                                                  17
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                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                               APPLICATION NUMBER:
                                                                                                         ELTSPVVAESP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK
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                                                      KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK
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                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                                                                                                                    33.78;
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                                                                                                                                                                                                                      Score 928; DB 1
Pred. No. 4e-59;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith & Reynolds, P.C
                                                                                                                                                                                                                                                  DB 1; Length 210;
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                                                                                                                                                                                                                     Gaps
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US-08-209-603E-15; Sequence 15; Application; Patent No. 6248538; GENERAL INFORMATION:
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US-08-235-836C-122
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Patent No.
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Best Local S
Matches 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNLS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Dunn, John J.
APPLICANT: Dunn, J.
APPLI
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acid
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                         466
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                                                                                                                                                                                                                                                                                                                      184 SPVVAESPAMGSNSGKGGDSASTN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 KIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 405
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STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Brookhaven National Laboratory
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                                                                                                                                                                                                                                                     SPVVAESPK-----KPGTMAQYN
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5. 6248562
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Pred. No. 4.3e-58;
Pred. No. 4.3e-58;
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; PUBLICATION INFORMATION:
US-08-209-603E-15
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILLEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 210
TYPE
                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: DSM 5662
POSITION IN GENOME: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9217-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
                          137 KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: L
MOLECULE TYPE:
                                                 121 KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 0
FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLC
COMPUTER: AT&T - IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-D
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PRITITLE OF INVENTION: FROM BORRELIA BURGDORFERI NUMBER OF SEQUENCES: 15
                                                                                                               61 IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETETN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                        77
                                                                                                                                                              17 ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVLEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION: PRODESCRIPTION: N/A
                                                                                                                                                                                TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/209,603E FILING DATE: 10-MAR-1994 CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                             IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10016
                                                                                                                                                                                                                                       Conservative
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99 PARK AVENUE
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PREAC-MURSIC, VERA
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97.9%;
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                                                                                                                                                                                                                                                   Score 921; DB 4;
Pred. No. 1.3e-58;
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                 Length 210;
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US-08-235-836C-34; Sequence 34, Application US/08235836C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08,
APPLICATION NUMBER: US 08,
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, VGURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,836C FILING DATE: 29-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                456
                                                                                                                               184 SPVVAESP 191
                                                                                                                                                                    396
                                                                                                                                                                             124 EKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT 183
                                                                                                                                                                                                                                        336
                                                                                                                                                                                                                                                                                                  STATE: NV
                                                                                                                                                                                                                                                  64 KIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 123
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                             AKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT
                                                                                                                                                                                                                             KIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 395
                                                                                              SPVVAESP
                                                                                                                                                                                                                                                                                                                                                                               186;
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            33.3%;
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INFORMATION: 6248562

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US-08-158-353-4
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                                                                                                     Sequence 4, Application US/08158353 Patent No. 5620862
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Best Local Similarity
Matches 187; Conserv
                              GENERAL INFORMATION:
APPLICANT: Padula,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (516) 282-3729 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BN
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/1
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: Bogostan, Margaret C.
REGISTRATION NUMBER: 25,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,8:
FILING DATE: 29-APR-1994
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APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising

TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
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PRIOR APPLICATION DATA:
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NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                             375
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                                                                                                                                                                                                                                                                                                                                                                 255 QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK 314
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 11973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Upton
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                                                                                                                                                                                                                                         LGHRNNSGGDSASTNP--DESAKGP 397
                                                                                                                                                                                                                                                                                                LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE 374
                                                                                                                                                                                                                                                                                                                                               QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK 139
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                                                                   Padula, Steven J.
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                           -TSPVVAESPKKP 212
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                              Methods for Diagnosing
Disease
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Pred. No. 2.4e-56;
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                                                Early Lyme
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US-08-235-836C-36
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Best Local S
Matches 186
                                                                                                                                                                                                                                  Patent No. 6248562
GENERAL INFORMATION:
                                                                                                                                                                                                                                                     Sequence 36, Application US/08235836C Patent No. 6248562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
COUNTRY: USA
ZIP: 11973
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Reli
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                      APPLICANT: Dunn, John J. APPLICANT: Luft, Benjamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                             CORRESPONDENCE ADDRESS:
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: Two Militia Drive
CITY: Lexington
                                                                                             CITY: Upton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                              STATE:
                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                          ADDRESSEE: Brookhaven National Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                            LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186;
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                                                                                                                                                                   No. 6248562el Chimeric Proteins Comprising
Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.2%;
90.7%;
                                                                                                                                                           144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33,542
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Pred. No. 4e-56;
2; Mismatches
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CURRENT APPLICATION NUMBER: US/09/196,293
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER FILING DATE: 1994-03-10
EARLIER FILING DATE: 1994-03-10
EARLIER FILING DATE: 1994-03-10
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER FILING DATE: 1990-06-13
NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                   APPLICANT: Fuchs, Renate
APPLICANT: Motz, Manfred
APPLICANT: Motz, Manfred
APPLICANT: Soutscheck Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
TITLE OF INVENTION: Active proteins from Borrelia
FILE REFERENCE: 738,001US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 181;
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Best Local (
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TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equence 11, Application US/09196293
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ATTORNEY/AGENT INFORMATION:
NAME: Bogosian Marcanat
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LENGTH: 207 amino acid:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           559 VA 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499 AELGIQSVQDDNAKKAILKTHGTKDKGAKELEELFKSLESLSKAAQAALTNSVKELTNPV 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 NDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSQKFTTKLKDSH 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 NNSGGDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAIGKKIK 438
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REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 29-AF
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SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSEKFTTKLKDSH 139
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Windows Version 4.0
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99.5%;
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LENGTH: 212
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Best Local Similarity
Matches 182; Conserv
                   TELEFAX: (212) 557-56
INFORMATION FOR SEQ ID NO:
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TYPE: PRT
                                               REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
SEQUENCE CHARACTERISTICS:
                                                                                         FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
BEFERBACE/DOCUMENTALINATION
                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/:
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 0
                                                                                                                                                                                                                                                                  COMPUTER: AT&T - IBM COMPATIBLE OPERATING SYSTEM: MS-DOS Version SOFTWARE: ASCII CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: IMMUNOLOGICALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: BROOKE AVENUE
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                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U:
ZIP: 10016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOUTSCHECK, ERWIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PREAC-MURSIC, MOTZ, MANFRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WILSKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUCHS, RENATE
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             557-5635
NO: 11:
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                                                                                                                                                             us 07/862,535
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Pred. No. 3.9e-54;
2; Mismatches 7;
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MOLECULE TYPE:

TOPOLOGY: LINEAR

DESCRIPTION: PROTEIN

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                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08158353
Patent No. 5620862
GENERAL INFORMATION:
APPLICANT: Padula, Steven J.
TITLE OF INVENTION: Methods for
TITLE OF INVENTION: Disease
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: CAITOII, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UCT9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617.861-6240
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st Local Similarity 88.8%;
tches 182; Conservation
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
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ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
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LIBRARY: DSM 5662
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                CITY: Lexington
                                                                                                                                                                                                                                                  ZIP: 02173
                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE 374
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                                                                                                                                                                                                                                                                                                                    Two Militia Drive
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NVENTION: Methods for Diagnosing Early Lyme

NVENTION: Disease
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                                                                                                                                                                                                                                                                   USA
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                                                                                                                                     US/08/158,353
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                                     JCT93-05
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                                                                                                                                                                                                                                                                                                                                  Smith & Reynolds,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08031295 Patent No. 5530103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                 PILING DATE: 25-JUN-1992

PRIOR APPLICATION NUMBER: US 07/824,161

APPLICATION NUMBER: US 07/824,161

PILING DATE: 22-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/727,245

FILING DATE: 11-JUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US,
FILING DATE: 1930312
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LIVEY, IA
APPLICANT: DORNER, F
TITLE OF INVENTION:
TITLE OF INVENTION:
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
TELEX: 904126
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKLKSSHAELGIANGAATDANAKAAILKTNGTKDKGAQELEKLFESVKNLSKAAQETLNN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETFT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGNLIAQ-NGLNAGANQNGSLLAGAYVISTLIAEKLDGLKNSEELKEKIEDAKKCNKAFT 135
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                                                                                                                                                                                                                                                      JMBER: US 07/903,580
25-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHOD AND COMPOSITION FOR THE PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.6%; Score 676; DB 1; 74.7%; Pred. No. 3.7e-41;
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                                                                      30472/142 IMMU
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 212 amino acid

2:

H: 212 amino acids
AMINO ACID

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RESULT 15
US-07-903-580-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/07903580
Patent No. 6221363
GENERAL INFORMATION:
APPLICANT: LIVEY, Ian
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND COMPOSITION FOR THE
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/824,161
FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,245
FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 142;
                                                                               NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 212 amino acids
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,580
FILING DATE: 19920625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 VKELTSPVVAESP 191
|||||||||||
197 VKELTSPVVAETP 209
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                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1800 Dia
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 AIGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEG-LKEKIDAAKKCSETF 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MACNNSGKDGNT-SANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAK 59 ::||||||| |::|||||:||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIGKKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDF 136
                                                                  899149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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73.6%;
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                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-07-903-580-2
                                                                                                                                                                                                                                                                                            Query Match 24.0%;
Best Local Similarity 73.6%;
Matches 142; Conservative 1
                 179 VKELTSPVVAESP 191
                                                                         137
                                                                                           119 TNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                   77
                                                                                                                                                                                                                   17 ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATK 76
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                    60 AIGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEG-LKEKIDAAKKCSETF 118
                                                                                                                                                                                                                                            1 MACNNSGKDGNT-SANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAK 59
VKELTSPVVAETP 209
                                                                       TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS 196
                                                                                                                                               AIGKKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDF 136
                                                                                                                                                                                                                                                                                            ; Score 661; DB 4; I
; Pred. No. 4.4e-40;
14; Mismatches 35;
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Search completed: March 18, 2002, 09:55:36 Job time: 349 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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IG 79 IG 79 IG 79 II 314 II 139 II 139 II 199 II 199	Gaps		4824, Ap. 12713, F. 12713, F. 19882, F. 3731, Ap. 3731,

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CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DX97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 5
LENGTH: 211
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TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEO ID NOS: 40
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US-09-974-992-3
                    Query Match
Best Local Similarity
      Matches 148;
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Best Local Similarity 98.9%;
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APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
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ORGANISM: Borrelia burgdorferi
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APPLICANT: BRILES et al.

APPLICANT: BRILES et al.

TITLE OF INVENTION: AND STRAINS THEREOF AND USES THER

FILE REFERENCE: 454312-3140

CURRENT APPLICATION NUMBER: US/09/748,875

CURRENT FILING DATE: 2000-12-26

PRIOR APPLICATION NUMBER: 09/298,523

PRIOR FILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 78

SOFTWARE: Patentin Ver. 2.1

TYPE: PAT

ORGANISM: Streptococcus pneumoniae

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Pred. No. 4.2e-07;
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URRENT APPLICATION NUMBER: US/09/748,875
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 60
LENGTH: 929
TYPE: PAT
ORGANISM: Streptococcus pneumoniae
US-09-748-875-60
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US-09-748-875-60
; Sequence 60, Application US/09748875
; GENERAL INFORMATION:
APPLICANT: BRILES et al.
: TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),
: TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
ILE REFERENCE: 454312-3140
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PNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAIGKKIKNDGTLDNEANRNESLIAG : |: | : | | | | | | | |
                                                     VKEEANESRNEEKIKQAKEKVES--KKAEATRLEKIKT---DRKKAEEEAKRKAEESEK-
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Pred. No. 6.3e-07;
4; Mismatches 260
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US-09-748-875-2
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Matches 139
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GENERAL INFORMATION:
APPLICANT: BRILES et al.
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CUGRENT APPLICATION NUMBER: US/09/748,875
CURRENT FILING DATE: 2000-12-26
BUTCH NUMBER: 2000-12-26
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PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
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TYPE: PRT
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                                          EAKQKVDAEEYAL----EAKIAELEYEVQRLEKELKEIDESDSEDYLKEGLRAPLQ--S
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                                                                                                                            NESRNEEKIKQAKEKVES--KKAEATRLEKIKT---DRKKAEEEAKRKAEESEK---KAA 499
                                                                                                                                                                 TTDKGAKEFKDLFESVEGLLKAAQVALTNSVKELGHRNNSGGDSASTNPDESAKGPNLTV 401
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22.2%; Pred. No. 7.7e-07;
tive 100; Mismatches 264;
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US-09-748-875-14
Sequence 14, Application US/09748875
GENERAL INFORMATION:
APPLICANT: BRILES et al.
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Matches 148; Conserv
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
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URRENT FILING DATE: 2000-12-26
RIOR APPLICATION NUMBER: 09/298,523
PRIOR FILING DATE: 1999-04-23
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TYPE: PRT
513 LQ--SKLDTKKAKLSKLEELSDKIDELDAEIAKLEVQLKDA---
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                                                                                          PNLTVISKKITDSNAFILAVKEVEALLSSIDELSKAIGKKIKNDGTLDNEANRNESLIAG 456
                                                                                                                                         VKEEANESRNEEKIKQAKEKVES--KKAEATRLEKIKT---DRKKAEEEAKRKAEESEK-
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                                                                   --KAAEAKQKVDAEEYAL----EÄKTAELEYEVQRLEKELKEIDESDSEDYLKEGLRAP
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-EGNNNVEAYF 561
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GENERAL INFORMATION:
APPLICANT: BRILES et al.
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/748,875
CURRENT FILING DATE: 2000-12-26
CURRENT FILING DATE: 2000-12-26
CURRENT FILING DATE: 2000-12-26
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SEQ ID NO 61
LENGTH: 690
TYPE: PRT
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Best Local
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KKAELEKAEADLKKAVDEPETPAPAPQPA 636
                                   THGTKDKGAKELEELFKSLESLSKAAQAA 546
                                                                    Q--SKLDTKKAKLSKLEELSDKIDELDAEIAKLEVQLKDAEGNNNVEAYFKEGLEKTTAE
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Pred. No. 1.9e-06;
Pred. Mismatches 263;
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US-09-748-875-62
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CURRENT APPLICATION UNMEER: US/09/748,875
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR PILING DATE: 1999-04-23
NUMBER OF SEO ID NOS: 78
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 62
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GENERAL INFORMATION:
APPLICANT: BRILES et al.
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                               THGTKDKGAKELEELFKSLESLSKAAQAA 546
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RESULT

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US-09-748-875-63; Sequence 63, Application; GENERAL INFORMATION:

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CURRENT APPLICATION NUMBER: US/09/748/875

CURRENT FILING DATE: 2000-12-26

PRIOR APPLICATION NUMBER: 09/298,523

PRIOR FILING DATE: 1999-04-23

PRIOR FILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PATENTIN VET. 2.1

SEQ ID NO 3

LENGTH: 711

"TOTAL TOTAL THEREOF AND USES THEREFOR PRIOR PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.0%; Score 221; DB 5; Best Local Similarity 20.5%; Pred. No. 2.9e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 TSYNKANES-----QTEHRK-----AAKQVDEDIKKMLSEIQEYIKKMLSEIQLDKRKH 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 TSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIG-----KKIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VETLV---LSIDELAKKAIGQKIDNNNGLAAL------NNQNGSLLAGAYAIS
KEGLEKTTAEKKAELEKAEADLKKAVDEPETPAPAPQPA 646
                                            DDNAKKAILKTHGTKDKGAKELEELFKSLESLSKAAQAA 546
                                                                                             YLKEGLRAPLQ--SKLDTKKAKLSKLEELSDKIDELDAEIAKLEVQLKDAEGNNNVEAYF 607
                                                                                                                                         NRNESLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSQKFTTKLKDSHAELGIQSVQ
                                                                                                                                                                                        RKAEESEK---KAAEAKQKVDAEEYAL----EAKTAELEYEVQRLEKELKEIDESDSED
                                                                                                                                                                                                                                    INPDESAKGPNLIVISKKITDSNAFLLAVKEVEALLSSIDELSKAIGKKIKNDGTLDNEA 447
                                                                                                                                                                                                                                                                                                                                 TDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKELGHRNNSGGDSAS
                                                                                                                                                                                                                                                                                                                                                                                                                          TLITEKLSK-----LKNLEELKTEIAKAKKCSEEF----TNKLKSGHADLGKQDA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDEYIKKMLSEIQLDRRKHTQNVNLNIKLSAIKTKYLYELSVLKENSKKEELTSKTKAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ELTSPVVAESPAMGSNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKVESKKAEATRLEEIKTERKKAEEEAKRKAEESEKKAAEAKQKVDTKEQGKPKRRAKRG
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                                                                                                                                                                                                                                                                                     KVKKAELELVKEEANESRNEEKIKQAKEKVES--KKAEATRLEKIKT---DRKKAEEEAK
                                                                                                                                                                                                                                                                                                                                                                              TAAFEQFKKDTLKPEKKVAEAEKKVEEAKKKAKDQKEEDRRNYPTNTYKTLELEIAESDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----EGVTDAD 138
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US-09-708-427-19881

Sequence 19881, Application US/09708427

GENERAL INFORMATION:
ADPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
                                                                                                                        RESULT 12
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LENGTH: 670
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CURRENT PRICTON NUMBER: US/09/748,875

CURRENT FILING DATE: 2000-12-26

PRIOR APPLICATION NUMBER: 09/298,523

PRIOR FILING DATE: 1999-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                     525 GAKELEELFKSLESLSKAAQAA 546
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                                                                                                                                                                                                                                  TKKAKLSKLEELSDKIDELDAEIAKLEVQLKDAEGNNNVEAYFKEGLEKTTAEKKAELEK
                                                                                                                                                                                                                                                                                                                                 KITDSNAFLLAVKEVEALLSSIDELSKAIGKKIKNDGTLDNEANRNESLIAGAYEISKLI 464
                                                                                                                                                                                                                                                                                                                                                                   RNEEKIKQAKEKVES--KKAEATRLEKIKT--DDRKKAEEEAKRKAEESEK---KAAEAK 470
                                                                                                                                                                                                                                                                                                                                                                                           KGAKEFKDLFESVEGLLKAAQVALTNSVKELGHRNNSGGDSASTNPDESAKGPNLTVISK 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDVKVKEAELELVKEEAKPRNEEKIKQAKAKVESKKAEATRLEEIKTERKKAEEEAKRKA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTNKLKEKHTDLGK-----EGVTDADAKEAILKTNGT-----KTKGAEELGKLF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQN-----VNLNRKL----SAIQTKYLYELRVLKEKSKKEELTSNYPTNTYKTLELEIAE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDA-----AKKCSE----T 117
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; LOCATION: 1..1269;
OTHER INFORMATION: Xaa is any amino acid;
NAME/KEY: misc_feature;
LOCATION: 1..1269;
OTHER INFORMATION: Ceres Seq. ID 1836845
US-09-708-427-19881
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19881
LENGTH: 1269
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Best Local Similarity
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TYPE: PRT
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                                           521 TKDKGAKELEEL-FKSLESLSKAAQAALTNS-----VKEL
                                                                                              810 KAMEEFTSRDSEASSLTEKLRDLEGKIKSYEEQLAEASGKSSSLKEKLEQTLGRLAAAES
                                                                                                                                                                                              750 SIENDLKAAGLQESEVMEKLKSAEESLEQKGREIDEATTKRMELEALHQSLSIDSEHRLQ
                                                                                                                                                                                                                                               436 KIKND----GTLDNEA-----NRNESLIAGAYEISKLIT------QKLSVLNSEELK
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VNEKLKQEFDQAQEKSLQSSSESELLAETNNQLKIKIQEL
                                                                                                                                              KKIK-----EAKDCSQKFTT---KLKDSHAELGIQSVQDDNAKKAILKTHG------
                                                                                                                                                                                                                                                                                                  AALNIATENEKELTENLNAVTSEKKKLEATVDEYSVKISESENLLESIRNELNVTQGKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELSLTQSSARNSELEEDLRIALQKGAEHEDRANTTHQRSIELEGLCQSSQSKHEDAEGRL 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DL------GKQDATDDHAKAAILK--THA----TTDKGAKEFKDL------FESVEGLL 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTN------KLKSGHA 320
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449 220 389 181 Gaps

33;

276

969 520 809 477 435 689 385

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APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
FILE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8001-
SOFTWARE: Patentin version 3.1
SEQ ID NO 7646
LENGTH: 1881
TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
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LOCATION: (1881)..(1881)
OTHER INFORMATION: X-any amino acid
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NELTEATSELTKLQDNNQSLTEEIEKTKAALTKSSKDL 1478
                                                                                                                                 KLSVLNSEELKKKIKEAKDCSQKFTTKLKDSHAELGIQSVQDDNAKKAILKTHGTKDKGA 526
                                                                                                                                                                              EREKEVRDIQSQLAAKTTDWEKIKTTLDKVLKEKS--DLEKTNKESVDTLKKEV-----
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                                          KELEELFKSLESLS------KAAQAALTNSVKEL
                                                                                    -----ENLKKEISLLEDOKKDDTTKYKELAAQLETKTSNLDSTTMELEKTELELKKVR 1440
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Best Local Similarity
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TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF THE PRIOR FILING DATE: 2001-02-09
NUMBER OF THE PRIOR FILING DATE: 2001-02-09
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APPLICANT:
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TYPE: PRT
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1284 EKEINDLIRKL-----
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                                         QVALTNSVKELGHRNNSGGDSASTNPDESAKGPNLTV-ISKKITDSNAFLL-----
                                                                               KSLKHDIEDLKREKIKLE----TTLKENEETMFEKKEQLQVVNDKCKELEACLKKLTETK 1283
                                                                                                             NKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKE------FKDLFESVEGLLKAA 364
                                                                                                                                                                                                          -IDNNNGLAALNNQNGSLLAGAYAISTLITEKL---SKLKNLEELKTEIAKAKKCSEEFT 312
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Ohlsen, Karl L.
Zyskind, Judith W.
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Boone, Charles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Foulkes, J. Goro
Zamudio, Carlos
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-- EAAKSDHDTERKKLSLLIEDTKSESEKNVIKLNEQIEKLKG 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 144;
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NAME/KEY: misc_feature

LOCATION: 1.114

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1.114

OTHER INFORMATION: Ceres Seq. ID 1828629

US-09-708-427-15046
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: HEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION UNDER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 15046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 155; Conserv
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321 DLGKQDATDDHAK---AAILKTHATTDKGA----KEFKDLFESVEGL----
                                      436 EWEGSVLEKIEELSKVKESLVDKETKLQSITQEAEELKGREAAHMKQIEE----LSTANA 491
                                                                                                                                                                                                    316 DSLKSTVDSIQNEFENSKAGWEQKELHLMGCVKKSEEENSSSQEEVSRLVNLLKESEEDA 375
                                                                                                                                                                                                                                            180 KELTSPVVA-ESPAMGSNSG------KGGDSASTNPADESAKGPNLTEIS----
                                                                                                                                                                                                                                                                                                                         130 GKEGYTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKE-----ML---ANSV 179
                                                                                                                                                                                                                                                                                                                                                                 217 LDNE-----KAATSNIQNLLDQRTELSIELERCKVEEEKSKKDMESLTLALQEASTE- 268
                                                                                                                                                                                                                                                                                                                                                                                                                                              157 NAAQKEKIELLEKTIEAQRTDLEEYGRQVCIAKEEASKLENLVESIKSELEISQEEKTRA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1441 NELTEATSELTKLODNNOSLTEEIEKTKAALTKSSKDL 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 SCTNSSVEEWKNKVHELEKEVEESNRSKSSASESME----SVMKQLAELNHVLHETKSD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1336 EREKEVRDIQSQLAAKTTDWEKIKTTLDKVLKEKS--DLEKTNKESVDTLKKEV-----
                                                                                                                                                                                                                                                                                                                                                                                                        71 LDTEYNHNGSLLAGAYAISTLIKQKLD-GLKNEGLKEKIDAAKKCSETFTNKLKEKHTDL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 -----LAVKEVEALLSSIDEIA----AKAIGKKI-----HONNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARKEEEASLKNNLKVAEGEVKYLQETLGEAKAESMKLKESLLDKEEDLKNVTAEISSLR 435
                                                                              NQNGSLLAGAYAISTL---ITEKLSKLKNL----EELKTEIAKAKKCSEEFTNKLKSGHA 320
                                                                                                                                                           -----KKITDSNAFVLAVKEVETLVLSIDE------LAKKAIGQKIDNNN---GLAALN 267
                                                                                                                                                                                                                                                                                   -----SSEAKATLLVCQ------EELKNCESQVDSLKLASKETNEKYEKMLEDARNEI 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KELEELFKSLESLS------KAAQAALTNSVKEL 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -AVKEVEALLSSI------DELSKAIGKKIKNDGTLDNEANRNESLIAGAYEISKLITO 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ENLKKEISLLEDQKKDDTTKYKELAAQLETKTSNLDSTTMELEKTELELKKVR 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLSVLNSEELKKKIKEAKDCSQKFTTKLKDSHAELGIQSVQDDNAKKAILKTHGTKDKGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.6%; Score 209; DB 6; Length 1144;
21.8%; Pred. No. 3.1e-05;
ative 116; Mismatches 247; Indels 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                222
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DЪ
            Вb
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                                                                                                                                                                                                                                                                                                                               Вb
725 ETKLQISNHEKEE--LKERETAYLKKIEELSK-VQEDLLNKENELHGMVV 771
                           511 AKKAIIKTHGTKDKGAKELEELF-KSLESLSKAAQAALTNSVKELTNPVV
                                                                            667 TTLLKKAEELSEL--NESLYDKASKLQTVYQENEELRERETAYLKKIEELSKLHEILSDQ 724
                                                                                                              452 -SLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSQKFTTKLKDSHAELGIQSVQDDN 510
                                                                                                                                                          607 LVDNVANMQNIAEESKDLREREVAYLKKIDELSTANGTLADNVTNLQNISEENKELRERE
                                                                                                                                                                                              406 ITDSNAFLLAVKEVE-----ALLSSIDELSKAIGKKIKNDGTLDNEANRNE-----
                                                                                                                                                                                                                                      547 DIKEREVAYIKKIEELSVANESIVDKETKIQHIDQEAEEIRGREASHIKKIEELSKENEN 606
                                                                                                                                                                                                                                                                               361 -LKAAQVALTNSVKELGHRNNSGGDSAS--TNPDESA------KGPNLTVISKK 405
                                                                                                                                                                                                                                                                                                                                  492
                                                                                                                                                                                                                                                                                                                     SL----VDEATKLQSIVQESEDLKEKEAGYLKKIEELSVANESLADNVTDLQSIVQESK
                                          559
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Search completed: March 18, 2002, 09:58:37 Job time: 395 sec

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Run OM protein - protein search, using sw model 9:: March 18, GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd 2002, 09:56:49 ; Search time 68.77 Seconds (without alignments)
620.296 Million cell updates/sec

Title: Perfect score: US-09-596-746A-52 2750 MACNNSGKDGNTSANSADES....

....KAAQAALTNSVKELTNPVVA 560

Gapop 10.0 , Gapext 0.5

Scoring table: BLOSUM62

Searched: 219241 seqs, 76174552 residues

tal number of hits satisfying chosen parameters:

219241

Amum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

pir3:* pir4:* pir1:* pir2:*

Database :

PIR_68:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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928 33.7 921 33.5 886 32.0 887 31.9 877 31.8 846 30.3 847 31.8 847 31.8 848 30.3 848 30.3 849 29.0 794 29.0 798 29.0 799 29.0 790 28.6 757.5	Score Match
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G70218 G70218 S20543 S20543 S37727 S69919 S69921 140122 140129 S54188 S54191 S54198 S54198 S54198 S54197 140145 S70287 1401279 S69927 S69922	ID
outer surface	cription

45	44	42	41	40	39	38	37	36	3 5	34	33	32	31	30
634.5	635	646	652.5	653.5	653.5	656.5	657.5	661	665	665.5	666	666.5	666.5	667
23.1	23.4	23.5	23.7	23.8	23.8	23.9	23.9	24.0	24.2	24.2	24.2	24.2	24.2	24.3
203	212	212	211	191	180	193	193	212	190	209	194	211	193	194
21	. .	N	N	Ŋ	N	N	Ŋ	Ŋ	N	N	N	N	N	N
140108	T40142	140279	S69932	S70284	S54189	S70274	S70276	S70254	S70273	S69917	S70277	I40278	S70265	S70268
surface	outer surface prot	surface												

ALIGNMENTS

RESULT: outer surface protein C - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13:Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000 C;Accession: G70218; I40269; S37726; S70281 Sutton, G.G.; Clayton, R.; Lathigra, R.; R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997 B. W.

Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943
A;Accession: G70218
A;Status: nucleic acid sequence not shown; translation not shown

R; Fukunaga, M.; Hamase, A. A;Molecule type: DNA
A;Residues: 1-210 <KLE>
A;Coss-references: GB:AE000792; NID:g3253098;
A;Experimental source: strain B31 PIDN: AAC66329.1; PID:g2689901; TIGR: BB

J. Clin. Microbiol. 33, 2415-2420, 1995
A; Title: Outer surface protein C gene sequence analysis
A; Reference number: 140269; MUID:96025162 A; Accession: I40269 of. Borrelia burgdorferi sensu

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-210 <RES>

A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684
R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschek, Med. Microbiol. Immunol. 182, 37-50, 1993
A;Title: Genetic heterogenity of the genes coding for the outer surface protein C A;Reference number: S37726; MUID:93268136 Soutschek, ်ပ္ပ [F]

A; Reference number: A; Accession: S37726

A;Status: preliminary

A; Molecule type: DNA A; Residues: 1-210 <JAU>

A;Cross-references: EMBL:x69596; NID:g311391; PIDN:CAAA9306.1; PID:g311392 R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995 A;Title: Evidence for lateral transfer and recombination in OspC variation in Lyme A;Reference number: S70255; MUID:96296448 A;Accession: S70281

di

A;Status: nucleic acid sequence not shown

A; Molecule type: DNA

A;Residues: 19-210 <LIV>
A;Residues: 19-210 <LIV>
A;Cross-references: EMBL:L42887; NID:g858715; PIDN:AAB36995.1; PID:g1695212
A;Experimental source: strain Ip2

C; Genetics:

A;Gene: ospC C;Superfamily: Lyme disease spirochete surface protein C

of a

Borrelia burgdorferi gene encoding

immunoreactivity of Os

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C:Species: Borrelia burgdorferi (Lyme disease spirochete)

A:Variety: strain PKa
C:Date: 15-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-May-2000
C:Accession: S6927; S72669
R:Jauris-Heipke, S:; Liegl, G.; Preac-Mursic, V.; Roessler, D.; Schwab, E.; Sout
J. Clin. Microbiol. 33, 1860-1866, 1995
A:Title: Molecular analysis of genes encoding outer surface protein C (OspC) of
A:Reference number: I40047; MUID:95395018
A:Accession: S69927
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-210 <JAU>
A:Cross-references: EMBL:X69589
A:Experimental source: strain PKa
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference number:
Accession: S72669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ne: ospC
perfamily: Lyme disease spirochete surface protein
                  197
                                                    181 ELTSPVVAESP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surface protein C precursor - Lyme disease spirochete (strain cies: Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                          77
                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                               17
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                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                  ELTSPVVAESP
                                                                                      KLKDKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                                                                                                                                          IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIEAAKKCSETFTN 136
                                                                                                                                                                                                 IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                                                                                                                                                                                                                            ISCNNSGKDGNTSANSADESVKGFNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                                                                                   186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELTSPVVAESP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELTSPVVAESP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGKKIHONNGLDTEYNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188;
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 33.5%;
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98.4%;
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                                                                                                                                                                                                                                                                                                                                                                          Score 921; DB 2;
Pred. No. 3.2e-34;
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Pred. No. 1.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       February 1994
                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              Length 210
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C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Molecule type: DNA
A:Residues: 19-212 <LIV>
A:Cross-references: EMBL:L42883; NID:g858709; PIDN:AAB36991.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain PWudI
A; Note: the nucleotide sequence was submitted to the EMBI
R; Livey, I.; Glbbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A; Title: Evidence for lateral transfer and recombination
A; Reference number: S70255; MUID:96296448
A; Accession: S70275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X73624; NID:g313273; PIDN:CAA52003.1; PID:g313274
A;Experimental source: strain DK26:
R;Jauris-Heipke, S;, Liegl, G; Preac-Mursic, V.; Roessler, D.; Schwab, E.
J. Clin. Microbiol. 33, 1860-1866, 1995
A;Title: Molecular analysis of genes encoding outer surface protein C (Ospinion of Company). 140047; MUID:95395018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-212 <FUC>
A;Cross-references: EMBL:X62162; NID:g39392; PIDN:CAA44093.1; PID:g39393
A;Cheisen, M.; Frederiksen, B.; Lebech, A.M.; Vuust, J.; Hansen, K.
J.; Clin. Microbiol. 31, 2570-2576, 1993
A;Title: Polymorphism in ospC gene of Borrelia burgdorferi and immunoreac A;Reference number: I40105; MUID:94075528
A;Accession: I40107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence
A;Molecule type: DNA
A;Residues: 1-212 <JAU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-212 <JAU>
A;Cross-references: EMBL:X69590
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A; Residues: 1-205 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                              Matches 186;
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Best Local
200
                                      375
                                                                                  140
                                                                                                                                                                                 255 OKIDNNNGLAALNNONGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEETNK 314
                                                                                                                                                                                                                                                                                                     195
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                                                                  LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE
                                                                                           LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE
                               LGHRNNSGGDSASTNP--DESAKGP 397
                                                                                                                                                          QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK
                                                                                                                                                                                                                                            NNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKKAIG
                                                                                                                                                                                                                                                                   SNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKKAIG
                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyme disease spirochete surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source: strain JSB
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                            32.2%;
90.7%;
                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                     Score 886; DB 2;
Pred. No. 1.1e-32;
2; Mismatches 3
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not shown; translation not shown

Schwab, E.;

Soutschek

EMBL

Data

Library,

February 1994

'n

OspC

variation in

PID:g1695209

Length 212;

Indels

14;

Gaps

2

79

139

RESULT S37727

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outer surface protein C precursor - Lyme disease spirochete C:Species: Borrelia burgdorfer1 (Lyme disease spirochete) C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-May-2000 C:Accession: S37727 R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschek, Med. Microbiol. Immunol. 182, 37-50, 1993 A;Title: Genetic heterogenity of the genes coding for the outer surface protein C A;Reference number: S37726; MUID:93268136 A;Accession: S37727
                                                                                                                                                                                                                                                                                                                                                                                                                                R; Jauris-Heipke, S.; Liegl, G.; Preac-Mursic, J. Clin. Microbiol. 33, 1860-1866, 1995
A;Title: Molecular analysis of genes encoding A;Reference number: 140047; MUID:95395018
A;Accession: 869919
A:Status: nucleic acid sequence not shown; traplecule type: DNA esidues: 1-207 <JAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outer surface protein C precursor - Borrella garinii (strain PTrob)
C;Specles: Borrella garinii
A;Variety: strain PTrob
C;Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000
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A;Residues: 1-207 <JAU>
A;Cross-references: EMBL:X69595; NID:g311393; PIDN:CAA49305.1;
C;Superfamily: Lyme disease spirochete surface protein C
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                                                                                                                                                                                                                                                                 C;Superfamily: Lyme disease spirochete surface protein C F;1-18/Domain: signal sequence #status predicted <SIG> F;19-207/Product: outer surface protein C #status predict
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Best Local S
Matches 180
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Best Local Similarity
Matches 181; Conserv
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                                                                                                                                                                                                                                                                                                                                                                        the nucleotide sequence was submitted to the EMBL Data Library, January 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSQKFTTKLKDSH
                 NDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSQKFTTKLKDSH
                                                                                                    NNSGGDSASTNPDESAKGPNLTVISKKITDSNAFILLAVKEVEALLSSIDELSKAIGKKIK 438
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                                                                               NNSGGDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAIGKKIK
NDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKEKIKEAKDCSEKFTTKLKDSH
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1; Mismatches
                                                                                                                                                                 <u>ب</u>
                                                                                                                                                                                  Score 878; DB 2;
Pred. No. 2.4e-32;
                                                                                                                                                                   Mismatches
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L.8e-32;
hes 0;
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                                                                                                                                                                                                                                                                 predicted
                                                                                                                                                                                                     Length 207;
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                                                                                                                                                                   Indels
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C;Genetics:
A;Gene: ospC
C;Superfamily:

Lyme

disease spirochete surface

protein

A; Cross-references:

EMBL: X73626; NID: g313277; PIDN: CAA52005.1;

PID: 9313278

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outer surface protein C precursor - Borrelia afzelii (strain PBO)

(;Species: Borrelia afzelii

A;Varlety: strain PBO

C;Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000

C;Accession: S69921; 140047

R;Jauris-Helpke, S; Litegl, G; Preac-Mursic, V.; Roessler, D.; Schwab, E.;

J. Clin. Microbiol. 33, 1860-1866, 1995

A;Title: Molecular analysis of genes encoding outer surface protein C (OspC)

A;Reference number: 140047; MUID:95395018

A;Accession: S69921
                                                      R;Theisen, M.; Frederiksen, B.; Lebech, A.M.; Vuust, J. Clin. Microbiol. 31, 2570-2576, 1993
A;Title: Polymorphism in ospC gene of Borrelia burgda A;Reference number: I40105; MUID:94075528
A;Accession: I40122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-212 < JAU>
A;Cross-references: EMBL:X81521; NID:g804954; PIDN:CAA57241.1; PID:g804955
A;Experimental source: strain PBo
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Sej
                                                                                                                                                      outer surface protein C - Lyme disease spirochete (strain DK6) (fragment) C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-20;C;Accession: I40122; S34177
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C; Superfamily:
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A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-200 <RES>
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Best Local Sim
Matches 184;
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Pred.
                                        from GB/EMBL/DDB:
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No. 2.
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f
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Length 200

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C;Species: Borrella afzelli
C;Date: 08-ul-1995 #sequence_revision 21-Jul-1995
C;Accession: 140115; S54187
R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelse
J. Bacteriol. 177, 3036-3044, 1995
A; Molecule type: I
A; Residues: 1-179
                                                                                                  R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, J. Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrelia burgdorferi outer s
                                              A;Accession: I40115
A;Status: translated from GB/EMBL/DDBJ
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A;Title: Evolution of the Borrelia burgdorferi outer s A;Reference number: 140104; MUID:95286481
A;Accession: 140129
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                    A; Reference number:
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C;Superfamily: Lyme disease
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A; Residues: 1-177 < RES>
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Best Local
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Best Local Similarity
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                                                                                    I40104;
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                                                                                                                                                                                                            Borrelia afzelii (strain DK2) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.0%;
98.9%;
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98.9%;
                                                                                  orrelia burgdorferi
MUID:95286481
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Pred. No. 2.5e-31;
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                                                                                                outer surface protein OspC
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outer surface protein C - Borrelia afzelii (strain DKG C;Species: Borrelia afzelii C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #te C;Accession: I40119; 554191 R;Thelsen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, J. Bacteriol. 177, 3036-3044, 1995 A;Title: Evolution of the Borrelia burgdorferi outer s
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S54191
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A; Residues: 1-179 <THE>
A; Cross-references: EMBL: X84771; NID: 9793803; PIDN: CAA59242.1;
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C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995
C;Accession: I40116; S54188
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C;Superfamily:
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S54188
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A;Status: translated from
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A;Title: Evolution of the Borrella burgdorferi outer surface protein OspC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain
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                                                                                                                                                                                                                                                                  GLAALNNONGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNKLKSGHAD
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99.4%;
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Pred. No. 5.1e-31;
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5.3e-31;
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                              B.; Lebech, A.M.; Hansen,
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surface

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C:Species Borrella afzelii
C:Acession: I40114; S54186
R:Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, A.M.; Hans
J. Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrella burgdorferi outer surface protein OspC.
A;Reference number: I40104; MUID:95286481
A;Status: translated from GB/EMBL/DDBJ
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C; Superf
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outer surface protein C · Lyme disease spirochete (strain C:Species: Borrella burgdorferi (Lyme disease spirochete) A:Varlety: strain KLll C:Date: 12-Feb-1998 #sequence_revision 26-Feb-1998 #text_C
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S70263
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A; Residues: 1-179 <THE>
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Best Local Similarity
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                                                                                                                                     DSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKKAIGQKIDNNN
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Pred. No. 2.1e-30;
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Pred. No. 1.7e-30;
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outer surface protein C precursor - Borrelia garinii C;Species: Borrelia garinii C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change C;Accession: 140271 R;Fukunaga, M.; Hamase, A. J. Clin. Microbiol. 33, 2415-2420, 1995 A;Reference number: 140269; MUID:96025162 A;Accession: 140271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain KL11 R; Livey, I.; Gibbs, C.P.; Schuster, submitted to the EMBL Data Library, A; Reference number: S77616 A; Accession: S77616
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R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination
A;Reference number: S70255; MUID:96296448
A;Accession: S70263
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A;Residues: 1-110,'E',112-117,'R',119-189 <LIW>
A;Cross-references: EMBL:L42880; NID:g858707; PIDN:AAB36989.1; PID:g1695207
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C;Superfamily: Lyme
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Residues: 1-207 <RES>
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C;Species: Borrelia garinii
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Dec-2000
C;Accession: 140126; S54198
R;Meisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, A.M.; Hansen, K.
acteriol. 177, 3036-3044, 1995
Letteriol. 177, 3036-3044, 1995
A;Reference number: 140104; MUID:95286481
A;Accession: 140126
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-200 <THE>
A;Cross-references: EMBL:X84781; NID:g793819; PIDN:CAA59252.1; PID:g793820
A;Note: submitted to the EMBL Data Library, February 1995
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SCA4_RICPR
REST_HUMAN
ZIP1_YEAST
BAG_STRAG
CAGA_HELPJ
SCI1_CHOUS
XJH6_YEAST
MYH3_CHOUS
YHGE_BACSU
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-!- FUNCTION: NOT KNOWN; MAJOR
-!- SUBCELLULAR LOCATION: ATTAC
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N-ACYL DIGLYCERIDE (BY SIMI C206C231FBF2E7D4 CRC64;
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-1- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPORTED
SEQUENCE FROM N.A.
STRAIN-SSP. HS1 SEROTYPE 3;
MEDLINE-93133110; PubMed-1484486;
Restrepo B.I., Kitten T., Carter C.J., Infante D., Barbour A.G.;
"Subtelomeric expression regions of Borrelia hermsii linear plasmids
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ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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N-ACYL DIGLYCERIDE
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Pred. No. 4.9e-11;
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CRC64;
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Plasmid.
SIGNAL 1 18 VARTABLE
CHAIN 19 215 VARTABLE
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            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                  Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                          HYPOTHETICAL SPAC1F3.06C.
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. Microbiol. 6:3299-311(1992).
. FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
. SUBSCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRAN
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Bioinformatics Institute.
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Best Local
USOL YEAST STANDARD; PKI; 1/70 ....
P25386;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO
USO1 OR INTI OR VDL058W.
USO1 OR INTI OR VDL058W.
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Pred. No.
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984 95

CNNLSKEKEHISKELVEYKSRFQSHDNLV--AKLTEKLKSLANNYKDMQA--ENESLIKA

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Matches 143;
                                                                                                   Query Match
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CONFLICT
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Bai Y., Symington L.S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ data
Submitted (MAY-1996) FOR PROTEIN TRANSPORT FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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Kendrick K.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 782-1790 FROM N.A.
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MEDLINE=91185402; PubMed=2010462;
"""" A., Ogawa Y.,
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                   CNNSGKDG----
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DOMAIN: THE RODLIKE TAIL
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S0002216; USO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no restr
                                                                             Similarity
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21.4%;
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DISPENSABLE FOR THE PROTEIN FU
ASP/GLU-RICH (ACIDIC).
G -> E (IN REF. 2).
E -> K (IN REF. 2).
V -> I (IN REF. 2).
I -> V (IN REF. 2).
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R -> S (IN REF. 2).
R -> GCE2B216E9FD4818 CRC64;
                                                                         Score 207.5;
Pred. No. 0.
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                                                      Mismatches
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the European Bioinformatics Institute. The summer of the statement is not removed modified and this statement is not removed
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HUMAN RETICULOCYTE CELLS.
SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: MEMBRANE-BOUND.
             SWISS-PROT entry is copyright. It is produced through a collab-
een the Swiss Institute of Bioinformatics and the EMBL outst
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by non-profit institutions as long as its content is in
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E BINDING PROTEIN 1 PRECURSOR.
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RESULT 8

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"Complete nucleotide sequence and deduced polypeptide sequence nonmusele myosin heavy chain gene from Acanthamoeba: evidence ching in the realistic train."
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PIR; A27224; A27224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Acanthamoebidae;
                                                                                                                                                                                                                                                                                                                                                                                                [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acanthamoeba castellanii (Amoeba)
28 EISKKITDSNAVLLAVKEVEA----LLSSIDE-----IAAKAIGKKIHQNNGLDTEYNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REDETITIVE, SHOW CYCLES OF A 28 -RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEP. CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HIMGE AND JOINED BY A NONHELICAL TAILPIECE 1 THE REGULATORY PHOSPHORYLATION SITES RESIDE.

MISCELLANBOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIAN THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTIVE SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MLC-2).
                                                                                                                                                                                                                                                                                                                                                                    PF00612; IQ; 2.
PF00063; myosin_head; 1.
                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                               IPR001609;
                                                                                                                                  790
848
848
1227
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1660
766
                         Conservative
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1509
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1482
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                                                                                                                                                                    189
682
                                                                                                                                                                                                                                                                          789
                                   7.48;
                                                                                                                                                                                                                                                                          Actin-binding; ATP-binding; Calmodulin-binding; ion; Phosphorylation; Multigene family.

89 MYOSIN HEAD-LIKE.
                                                                                   171201
                                                                                                                                                                                                                                                                                                                                                                                            myosin_head
                         107;
                                                                                  ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acanthamoeba.
                                                                                          METHYLATION (TRI-) (POTENTIAL)
ALKYLATION (SH-1) (POTENTIAL).
PHOSPHORYLATION.
PHOSPHORYLATION.
PHOSPHORYLATION.
                                   Score 204.5;
Pred. No. 0.
                                                                                                                                                       ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                         ALPHA-HELICAL TAILPIECE NONHELICAL TAILPIECE
                                                                                                                                                                                                               LIGHT MEROMYOSIN (LMM)
                                                                                                                                                                                                                              HINGE
                                                                                                                                                                                                                                      COILED COIL (POTENTIAL). ALPHA-HELICAL TAILPIECE
                         Mismatches
                                                                                 2CE49BE51173D17E
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                                   .086;
                                              DB
                                                                                                                                                                                                    TAILPIECE (LMM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as its content
                       218;
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                                              1;
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Q99323;
Q1-JUN-1994
                                                                             Ketchum A.S., Stewart C.T., Stewart M., Kiehart D.P.;
"Complete sequence of the Drosophila nonmuscle myosin heavy-chai
transcript: conserved sequences in the myosin tail and different
splicing in the 5' untranslated sequence.";
Proc. Natl. Acad. Sci. U.S.A. 87:6316-6320(1990).
-!- FUNCTION: NONMUSCLE MYOSIN APPEARS TO BE RESPONSIBLE FOR
-!- CELLULARIZATION. REQUIRED FOR MORPHOGENESIS AND CYTOKINESIS.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) A
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthrope
Pterygota; Neoptera; Endopte
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1415
               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
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                                                                                                                                                                                                                                                    MEDLINE=90349606; PubMed=2117279;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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20-AUG-2001
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                                                          SIMILARITY: CONTAINS 1 MYOSIN-LIKE SIMILARITY: CONTAINS 1 IQ DOMAIN.
 European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGTKDKGAKELEELFK-----SLESLSK 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQLEEEQDAKSHADSSSRRLLAEIEELKKRVAKETSDKQKAQDQKANYQRENESLKA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKAAQVALTNSVKELGHRN-----NSGGDSASTNPDESAKGPNLTVISKKI-TDSNAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAQLTADLDAERDSGAQQRRKLNTRISELQSELENAPKTGGASSEEVKRLEGELERLEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNKLKS----GHADLGKQDATDDHAKAAIL-----KTHATTDKGAKEFKDLFESVEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEAKLTELEDQVTALDGQKNAAAAQAKTLKTQVDETKRRLEEAEASAARLEKERKNALDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDSLKSK----LSAAEKSLKTAKDQN-RDLDEQLEDE
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                                                                                                                                                                                                                                                                                                                                                   Metazoa; Arthropoda; Tra
Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                                                                                                      melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 29, Created)
(Rel. 29, Last sequence up
(Rel. 40, Last annotation
(CHAIN, NON-MUSCLE (ZIPPER
 Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                    (ZIPPER PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                   Tracheata; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                   Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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                                                                                                                                                                                                   nonmuscle myosin heavy-chain
he myosin tail and differential
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There
                                                                                                                                                                                                                                                                                                                                                   Brachycera;
 are
                                                                                                                                                                                                                                                                                                                                                                                                                    (MYOSIN II).
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            gh a collaboration EMBL outstation -
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outstation -
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Query Match
Best Local S
Matches 131
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VARSPLIC
SEQUENCE
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Pfam; PF0063; myosin_head; 1.
Pfam; PF01576; Myosin_tall; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
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NP_BIND
DOMAIN
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ELEDATIELEAQRTKVLELEKKQKNFDKILAEEKAISEQIAQERDTAEREAREKE-----
                                                                                        KEFKDLFESVEGLLKAAQ----VALTNSVKELGHRNNSGGDSASTNPDESAKGPNLTVISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTEISKKITDSNAVLL----AVKEVEALLSSID-----EIAAKAIGKKIHQNNGLDTEYN 76
                                  KITDSNAFLLA----VKEVEALLSSIDEL---SKAIGKKIKND-GTLDNEANRNESLIAG
                                                                 EEDADLAKELEEGKKRLNKDIEALERQVKELIAQND-----RLDKSKK-----KIQS
                                                                                                                                                                 KKCSEEFT------NKLKSGHADLGKQDATDDHAK-----AAILKTHATTDKGA
                                                                                                                                                                                                   EKCTK-LQQEAEN-----ITNQLEEAELKASA-----AVKSASNMESQLTEA
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                                                                                                                                                                                                                                                                    -EKAKGTLEAENADLATELRSVNSSRQEN--DRRRKQAESQIAELQVKLAEIERARSELQ
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SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002928; Myosin_tail.
IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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1 829 MYOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B36014.
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a license
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25 KDA/50 KDA JUNCTION.

50 KDA/20 KDA JUNCTION.

50 KDA/20 KDA JUNCTION.

ACTIN-BINDING.

REACTIVE SULFHYDRYL/ACTIN-BINDING.

LIGHT MEROMYOSIN (LMM).

ALPHA-HELICAL TAILPIECE (LMM).
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MISSING (IN SHORT ISOFORM).
MW; 73E3CB02BA8F2528 CRC64;
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| http://www.isb-sib.ch/announce/
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Smith C.A., Rayment I.;
"X-ray structure of the magnesium(II)-pyrophosphate
"X-ray structure of the magnesium(II)-pyrophosphate
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Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.; "X-ray structures of the MgADP, MgATPgammaS, and
                                                                                                         Smith C.A., Rayment I.;
"X-ray structure of the magnesium(II).
Dictyostellum discoideum myosin motor
Biochemistry 35:5404-5417(1996).
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                                          X-RAY CRYSTALLOGRAPHY (2.1 ANGST MEDLINE-97452580; PubMed-9305951
                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
MEDLINE-96206189; PubMed-8611530;
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MEDLINE=95345067; PubMed=7619796;
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MEDLINE-95345066; PubMed-7619795;
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Myosin; Coiled coil; Act
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PDB; 1VOM; 23-DEC-96.
PDB; 1LVK; 28-JAN-98.
PDB; DD01008; mhcA.
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J. Mol. Biol. 274:394-407(1997).
-I- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY ACTIN.
-I- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MIC), 2 ALKALLICHT CHAIN SUBUNITS (MIC), 2 ALKALLICHT CHAIN SUBUNITS (MIC), 2 ALKALLICHT CHAIN SUBUNITS
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InterPro; IPR001609; myosin_head.
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                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M14628; AAA33227.1;
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CORTEX.
DOMAIN: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN BE FURTHER SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CÓNTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION AND REDUCES THE ACTIV-ACTIVATED ATPASE ACTIVITY.

MISCELLANBOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EDTA ATPASE ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE OF A CYS AT THE SH-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
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1MMG;
1MMN;
1MND;
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S00250; S00250.
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IQ.
COILED COIL (POTENTIAL).
ATP.
ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (DI-) (POTENTIAL).
ALKYLATION (SH-1).
PHOSPHORYLATION (BY MHCK).
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                                                                                                                                                           REST_CHICK STANDARD; PRT; 1433 AA. 042184; 04228; 057563; 057564; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) RESTIN (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170).
                                                                                                                                             RESTIN
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                  Gallus.
NCBI_TaxID=9031;
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140; Conserv
                                                                                                                     gallus (Chicken)
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                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                     Galliformes;
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Best Local Similarity
Matches 137; Conserv
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"Identification and expression of two novel CLIP-170,
expressed predominantly in muscle.";

Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databas
-1- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASS
THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES (B)
-1- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WIT
CYTOSKELEFOON (BY SIMILARITY).
-1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS ARE PROAUTIONED CONTRACTIONED CONTRACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF014012; AAC60344.1; -.
EMBL; AF020764; AAC60345.1; -.
EMBL; AF045550; AAC03547.1; -.
EMBL; AF045551; AAC03548.1; -.
EMBL; AF045651; AAC03548.1; -.
InterPro; IPR000938; CAP-Gly.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF01302; CAP_GLY; 2.
SMART; SM00343; Znf_C2HC; 1.
PROSITE; PS00845; CAP_GLY_1; 2.
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griparic L., Volosky J.M., Keller T.C. III; "Cloning and expression of chicken CLIP-170 and restin isoforms.";
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SVEVLSKAAKEMLANSVKELTSPVVAESPAMGSNSGKGGDSASTNPADES--AKGPNLTE: | | : | | : | | : : | | : : |
                                                                       - VNQVKDSLEKELQLLKEKFTSAVDGAENAQRAMQETINKLNQKEEQFALMSSELEQLKS
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K -> R (IN F
E -> V (IN F
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Pred. No. 0.25,
98; Mismatches
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CCHC-BOX.
CCHC-BOX.
MISSING (IN SHORT ISOFORM).
TQTKLEHARIKELEQSLLFEKTKADKLORELEDTR ->
RKRQISEDPEN (IN ISOFORM CLIP-170(11)).
S -> GGSSKYS (IN ISOFORM CLIP-170(11)).
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V (IN REF. 2; AAC03548).
5631CE8683498E23 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN B (MHC B).
UNC-54 OR MYO-4.
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                                                                                                                 Waterston R.H.;
"The genes sup-7 X and sup-5 III of C. elegans nonsense mutations via altered transfer RNA.";
Cell 33:575-583(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
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                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=83273600; PubMed=6576334;
Karn J., Brenner S., Barnett L.;
"Protein structural domains in the Caenorhabditis elegans
myosin heavy chain gene are not separated by introns.";
Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
                                                                                                                                                                                Wills N., Gesteland
                                                                                                                                                                                                   SEQUENCE OF 1876-1966 FROM N.A. MEDLINE-83232892; PubMed-6571695;
                                                                                                                                                                                                                                                                                    McLachlan A.D., Karn J.; neriodic charge distributions in
                                                                                                                                                                                                                                                                                                                     MEDLINE=82272395; PubMed=7202124;
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FUNCTION: MUSCLE CONTRACTION.
SUBGUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS
SUBGUNIT: MUSCLE MYOSIN IS A LEXAMERIC PROTEIN SUBUNITS (M
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC-2).
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
AND 2 REGULATORY LIGHT CHAIN SUBUNITS OF THE MYOFIBRILS.
SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS. SHOW
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOW
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEE
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                                                                                                                                                                                                                                                                                                     Karn J
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CONFLICT
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SEQUENCE
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InterPro; IPR001609; myosin_head.
Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
                                       246
                                                                                              186
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PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN C.
                              DELAKKAIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAK-A
                                                                                     VVAESPAMGSNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSI
                                                                                                                                          LGKEGVTDADAKEAILKTNGT---KTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSP
                                                                                                                                                                                                  GLDTEYNHNGSL-LAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKEKHTD 128
                                                                                                                                                                                                                                                       SADESVKGPNLTEISKKITDSNAVLLAVK---EVEALLSSIDEI--AAKAIGKKIHQ-NN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAM SIMILARITY: CONTAINS I MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                               LAAE----LDGAQRDLRNTSTDLFKAKNAQE--ELAEVVEGLRRENKS-LSQEIKDLTDQ 1527
                                                                                                                                                                       ALDAANSKNASLEKTKSRLVGDLDDAQVDVERANGVASALEKKQKGFDKIIDEWRKKTDD
                                                                                                                                                                                                                            SLEEEIEGKN--EILRQLSKANADIQQWKARFEGEGLLKA-DELEDAKRRQAQKINELQE 1414
          -EIEKEELQHALDEAE--AALEAEESKYLRAQVEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELEGANS
                                                                                                                                                                                                                                                                                             127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00242; MYSC;
                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                     851
1165
1165
1165
177
665
769
128
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                              ₽
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US: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS
                                                                                                                                                                                                                                                                                                                                                                           1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1176
1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 850
1966
1164
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687
783
128
705
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                                                                                                                                                                                                                                                                                                                                                             225125
                                                                                                                                                                                                                                                                                       104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alkylation;
                                                                                                                                                                                                                                                                                      Score 192; DB
Pred. No. 0.39;
04; Mismatches
                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                  METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
E -> R (IN REF. 2).
I -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIGHT MEROMYOSIN (LMM).
ATP (BY SIMILARITY).
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYOSIN HEAD-LIKE.
COILED COIL (POTENTIAL).
ALPHA-HELICAL TAILPIECE
                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HINGE.
                                                                                                                                                                                                                                                                                                                                                           B66F0BB2FE27B67F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thick filament; Actin-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOUND EXCLUSIVELY IN THE
                                                                                                                                                                                                                                                                                                     DB 1;
).39;
                                                                                                                                                                                                                                                                                       213;
                                                                                                                                                                                                                                                                                                                Length 1966;
                                                                                                                                                                                                                                                                                    Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (S2).
       QIRSEIEKRI
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RESULT
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                               CONFLICT
CONFLICT
                                                                                                        Antigen;
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 11-1016 FROM N.A.

SEKEYOVA Z., ROUX V., RAOULT D.;
SEKEYOVA Z., ROUX V., RAOULT D.;
SEKEYOVA Z., ROUX V., RAOULT D.;
Phylogenetic analysis of Rickettsia spp. by comparing s
'Phylogenetic analysis of Rickettsia spp. by comparing s
'gene D' coding for an intracytoplasmic protein.";
Submitted (OCT-1999) to the EMBLYGenBank/DDBJ databases.

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund Eriksson A.-S., Winkler H.H., Kurland C.G.;

"The genome sequence of Rickettsia prowazekii and the crimitochondria.";
               SEQUENCE
                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCA4_RICPR STANDARD; PRT; 1022 AA. 092D49; 092D48; 09AJ36; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) ANTIGENIC HEAT-STABLE 120 KDA PROTEIN (PS120)
                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _RICPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=MADRID E;
MEDLINE=99039499; PubMed=9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCA4 OR RP498/RP499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=782;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMESHIFT IN POSITION 234.
                                                                                                                                                                              AJ235272;
AJ235272;
                                                                                                                                                            AF200340;
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          AΑ;
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CAA14950.1;
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                                                    365
413
          114410
EFDPL -> RPGLV (IN REF. :)
H -> Y (IN REF. 2).
MISSING (IN REF. 2).
G -> R (IN REF. 2).
0 MW; .03230E3A663A9622 CRC(
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eae; Rickettsia.
                                                                                                                                                                         ALT_FRAME.
ALT_FRAME.
                                                                                                                                                                                                                                                                            (See http://www.isb-sib
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Best Local S
Matches 158
                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RESTIN (CYTOPLASMIC LINKER PROTEIN-170 ALPHA-2) (CL
STERNBERG INTERMEDIATE FILAMENT ASSOCIATED PROTEIN)
                                                                                                                                                                                 REST_HUMAN P30622;
                                                                                                                                                                                                          HUMAN
SEQUENCE FROM N.A. TISSUE-Peripheral MEDLINE-92289675;
                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                         HOMO
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                                                                                        sapiens (Human)
                                                                                                                                                                                                                                                                                     KSLESLSKAAQ
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                                                                                                                                                                                                                                                              KAFDNKSSTEE
                                                                                                                                                                                                                                                                                                                 APKKVSSLLNDISKRTIEKINNLRAMLS---
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                                                                                                                                                                                                                                                                                                                                                                   EIQN----LDRELKAQNINESKLHDDIYNKTQDVANALKNVIT---TVLDDNSGQRGVSEE
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                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                        544
PubMed=1600942;
                                                               Chordata;
Primates;
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23.5%;
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Pred. No.
                                                               Craniata; Vo
Catarrhini;
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i; Hominidae;
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                                                                          Euteleostomi;
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Best Local :
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DOMAIN
VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000938; CAP-Gly.
InterPro; IPR001878; Znf_CCHC
Pfam; PF01302; CAP_GLY; Z.
SMART; SM00343; Znf_C2HC; 1.
PROSITE; PS00845; CAP_GLY_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bilbe G., Delable J., Brueggen J., Richener H., Asselbergs F.A.M., Cerletti N., Sorg C., Odink K., Tarcsay L., Wiesendanger W., de Wolf-Peeters C., Shipman R.; "Restin: a novel intermediate filament-associated protein highly expressed in the Reed-Sternberg cells of Hodgkin's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE)
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES -!- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92405160; PubMed=1356075;
Pierre P., Scheel J., Rickard J.E., Kreis T.E.;
"CLIP-170 links endocytic vesicles to microtubules.";
Cell 70:887-900(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S22695; S22695.
MIM; 179838; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X64838; CAA46050.1; EMBL; M97501; AAA35693.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoskeleton;
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                                         VIKEKENSLEAIRSKLDKAEDQHLVEMEDTLNKLQEAEIKVKELEVLQAKCNEQTKVIDN
                                                                                                                                                                               LLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKEK-HTDLGKEGVTDADA 139
                                                                                                                                                                                                          ESNKPAGDVDMSLSLLQEISSLQEKLE-----VTRTDHQREITSLKEHFGAREETHQKE
                                                                                                                                                                                                                                    EISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHQNNGLD-----TEYNHNGS
                                                                                               KVSFSKGLGTETAEFAELKTQIEKMRLDYQHEIENLQNQQDSERAAHAKEMEALRAKLMK
                                                                                                                        KEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVVAESPAMGSN---
                                                                                                                                                     IKALYTATEKLSKE-----NESLKSKLEHANKENSDVIALWKSKLETAIASHQQAMEEL
                                                                                                                                                                                                                                                                 135;
                                                                    SGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAK----
                                                                                                                                                                                                                                                                             Similarity
 KAIGQKI-----
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143
214
304
350
1408
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204
279
279
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100;
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SER RICH.
COILED COIL (POTENTIAL).
CCHC-BOX.
MISSING (IN SHORT ISOFORM).
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SER-RICH.
CAP-GLY 2.
                                                                                                                                                                                                                                                                             Score 189;
Pred. No. 0.
                                                                                                                                                                                                                                                                 Mismatches
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OA4F166DD94254E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                            coil;
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                                                                                                                                                                                                                                                                 249;
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               284
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δÃ 밁

В

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RESULT 15
ZIP1_YEAST
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-I- FUNCTION: REQUIRED FOR MEIOTIC CHROMOSOME SYNAPSIS AND CELL CYCLE PROCRESSION. MAY ACT AS A MOLECULAR ZIPPER TO BRING HOMOLOGOUS CHROMOSOMES IN CLOSE APPOSITION. ZIPI MAY ENCODE THE TRANSVERSE FILAMENTS OF THE SYNAPTONEMAL COMPLEX.
use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sym M., Engebrecht J.A., Rooder G.S.;
"ZIPI is a synaptonemal complex protein required chromosome synapsis.";
(cell 72:365-378(1993).
[2]
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MEDLINE-93161412;
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P31111;
01-JUL-1993 (Rel. 26, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
SYNAPTONEMAL COMPLEX PROTEIN ZIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S288C
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EMBL; U51031; AAB64474.1;
PIR; A45173; A45173
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SGD; S0002693; ZIP1
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--LESLEEVTKNLQQKVQSQKRELEQKIKEL
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                                                                                     SEELKKKIKEAKDCSQKFTTKLKDSHAELGI--QSV-----QDDNAKKAILKTHGTKD 523
                                                                                                                ALVSENDTLKQRIQQLVEIKENEQKDHTTKLEAFQKNNEQLQKLNVEVVQLKAHEL----
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                                                                                                                                                                          SQISGKEQSLTEKNENLSNELKKVQDQLEKLNNLNITTKSNYENKISSQNEI-----VK
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MW; 674F12625CD9DDFD CRC64;
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EMBL; L42887; AAB36995.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
Lyme disease Borrella.";
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STRAIN=IP2;
                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                                                MEDLINE=96296448; PubMed=8709845;
                                                                                                                                                                                                                                                                                    NCBI_TaxID=139;
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123
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                                                      KEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL 182
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192 AA;
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20287 MW;
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99.58;

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Spirochaetaceae; Borrelia
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Pred. No. 3.
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U91798; AAB81895.1;
InterPro; IPRO01800; Lipoprotein_6.
Pfam: PF01441; Lipoprotein_6; 1.
ProDom: PD001149; Lipoprotein_6; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence updat
01-JUN-2001 (TrEMBLrel. 17, Last annotation upd
OUTER SURFACE PROTEIN C (FRAGMENY).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borr
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"Borrelia burgdorferi sensu stricto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97478003; PubMed=9336916;
Ras N.M., Postic D., Foretz M., Baranton G.
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Best Local Similarity
                                                                                                                Matches 184;
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Best Local
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                     InterPro; IPR01809; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
Probom; PD001149; Lipoprotein_6: 1.
                                                                                                                                                                                                                                                                                                           MEDLINE=99091544; PubMed=9872945; Wang I.N., Dykhuizen D.E., Qiu W., Dunn "Genetic diversity of ospc in a local pc burgdorferi sensu stricto."; Genetics 151:13-30(1999).

TEMBL: AF029860; AAB86543.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi
Bacteria; Spirochaeta
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ProDom; PD001149; Lipoprotein_6; 1.
NON_TER 1
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IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                   ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA
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186; Conserv
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98.4%;
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98.9%;
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                                                                                                          Score 908; DB 2;
Pred. No. 2.6e-34;
2; Mismatches 1
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Pred. No. 2.1e-34;
""" watches 2;
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Best Local Sim
Matches 181;
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                                                                                                        Q9S3P4;
Q9S3P4;
Q1-MAY-2000
                                        01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
OUTER SURFACE PROTEIN C (FRA
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER SURFACE PROTEIN C PRECURSOR (FRAGMENT).
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Bacteria; Sp
  Borrelia
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Hofmeister E.K., Glass G.E., Childs
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NCBI_TaxID=139;
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  disease spirochete)
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Pred. No. 1.
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Best Local Similarity
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                                          NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                  STRAIN-TETS;
Marti-Ras N., Postic D., I
Submitted (MAR-1997) to tl
EMBL; U91797; AAB81894.1;
                                                                                                                                                                                                                                                                                                                        MEDLINE=97478003; PubMed=9336916;
Ras N.M., Postic D., Foretz M., Be
"Borrelia burgdorferi sensu strict
U.S.A.'?";
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NON_TER
SEQUENCE
                                                                                                        InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9R7B2;
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                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      Int. J. Syst.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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ProDom; PD001149; Lipoprotein_6;
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Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96296448;
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182 /
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194 i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                             182
; 19202 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSPVVAESPKKP
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20446 MW;
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90.7%;
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                                                                                                                                                                                                                    Foretz M.,
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No. 2
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Spirochaetales; Spirochaetaceae; Borrelia
                                                                                              CEEDC9FA5DF0D68F CRC64;
                                          Mismatches
                                                                                                                                                                                               Dorner F.; recombination
                                                    DB 2;
.5e-33;
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                                                              Length
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                                          Indels
                                                                                                                                                                                               OspC variation
                                         Gaps
61
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LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK 314 SNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKKAIG QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK NNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKKAIG

374

121

01-MAY-2000 (TrEMBLrel 13, Created)
01-MAY-2000 (TrEMBLrel 13, Last sequence up
01-JUN-2001 (TrEMBLrel 17, Last annotation
OUTER SURFACE PROTEIN C (FRAGMENT) 47:1112-1117(1997) spirochaetaceae; Borr M., Baranton G. stricto, a bact EMBL/GenBank/DDBJ databases 422146F99AA57BF2 CRC64; Baranton a bacterial ş Borrelia update) ດ species 'made

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Query Match
Best Local Similarity
Matches 180; Conserv
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PNBLIFF.

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P96507:
P96507:
P16507:
P1650
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Masuzawa T., Sawaki K., Yoshii T.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; AB000345; BAA19078.1;
EMBL; AB009895; BAA24125.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BFOX;
Masuzawa T., Komikado
Submitted (JAN-1997) t
                                      194
                                                                  375
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Bacteria; Spiroch
                                                                                                                                  315
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                                                                                                                                                                                              255
                                                                                                                                                                                                                  Bacteria; Spirochaetales;
NCBI_TaxID=29518;
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ilarity 99.4%;
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21549 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Fukui
the EMBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ukui T., Yanagihara
EMBL/GenBank/DDBJ (
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Pred. No. 3.3e-33;
1; Mismatches 0
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                  94A885FBBACFE1C4 CRC64;
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.6e-33;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilske B., Preace-Mursic V., Jauris S., Pradel I., Sout Schwab E., Wanner G.;

"Inmunological and molecular polymorphisms of OspC, an major outer surface protein of Borrelia burgdorferi.";

Infect. Immun. 61:2182-2191(1993).

EMBL; X65595; CAA49305.1;

InterPro; IPR001800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

SEQUENCE 207 AA; 22320 MW; 4A525ABDAE63B5C8 CRC64;
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Q9KIM4;
01-OCT-2000
01-OCT-2000
01-JUN-2001
                                    NCBI_TaxID=29518;
                                                   Borrelia afzelii.
Bacteria; Spiroch
                                                                                      OSPC
                                                                                                  OUTER SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93268136; PubMed-8098841; Jauris-Heipke S., Fuchs R., Motz M., Preac-Murs Will G., Wilske B.; "Genetic heterogenity of the genes coding for t: protein C (OspC) and the flagellin of Borrelia Med. Microbiol. Immunol. 182:37-50(1993).
                                                                                                                                                                                                                                                               200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379
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                                                                                                                                                                                                                                                             ٧A
                                                                                                                                                                                                                                                                                  - VA
                                                                                                                                                                                                                                                                                                                     AELGIQSVQDDNAKKAILKTHGTKDKGAKELEELFKSLESLSKAAQAALTNSVKELTNPV
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                                                                                                                                                                                                                                                                                                                                         AELGIQSVQDDNAKKAILKTHGTKDKGAKELEELFKSLESLSKAAQAALTNSVKELTNPV 558
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                                                   Spirochaetales;
                                                                                               (TrEMBLrel. 1) (TrEMBLrel. 1) (TrEMBLrel. 1) (TrEMBLrel. 1)
                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
     N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.0%;
99.5%;
                                                                                                               15,
15,
17,
                                                Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 881; DB
; Pred. No. 4.6e
1; Mismatches
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Spirochaetaceae; Borr
                                                                                                              Created)
Last sequence up
Last annotation
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.6e-33;
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ database:
EMBL; AF230185; AAF75626.1; -.
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
SEQUENCE 212 AA; 22495 MW; C51DAF803BF2E7D4 CRC64;
                                                                                                                                                                                                     Jauris-Heipke S., Liegi G., Preac-Mursic V., Roessle Soutschek E., Will G., Wilske B.; "Molecular analysis of genes encoding outer surface of Borrelia burgdorferi sensu lato: relationship to evidence of lateral gene exchange of ospC."; J. Clin. Microbiol. 33:1860-1866(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95213332; PubMed-7699024; Wilske B., Jauris-Helpke S., Lobentanzer R., Pradel I., Wilske B., Jauris-Helpke S., Lobentanzer R., Pradel I., Pradel I., Seac-Mursic V., Rossler D., Soutschek E., Johnson R.C.; "Phenotypic analysis of outer surface protein C (OspC) of Borrelia burgdorferi sensu lato by monoclonal antibodies: relationship to genospecies and OspA serotype."; "J. Clin. Microbiol. 33:103-109(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia garinii.
Bacteria; Spirochaetales;
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Dykhuizen D.E.,
STRAIN-PSCF, PBAEII, PFIN, PFLK, PMUE, PSH; Marconi R.T., Hohenberger S., Jauris-Heipke S., Schulte-Spechtel Lavole C.P., Roessler D., Wilske B.; Lavole C.P., Roessler D., Wilske B.; "Genetic analysis of B.garinii OspA-serotype 4 strains associated neuroborreliosis: evidence for extensive genetic homogeneity."; submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                         STRAIN-PTROB; PubMed-7665660;
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EMBL; AJ123795; CAB46233.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom: PD001149; Lipoprotein_6; 1.
SEQUENCE 207 AA; 22249 MW; 20889AA7
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ
EMBL; AB009899; BAA24129.1; -.
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OUTER SURFACE PROTEIN C
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Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

SEQUENCE 212 AA; 22514 MW; C6EDC33BFD488DDE
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"Molecular analysis of genes encoding outer surfa of Borrelia burgdorferi sensu lato: relationship evidence of lateral gene exchange of ospC.";
J. Clin. Microbiol. 33:1860-1866(1995).
EMBL; X81521; CAA57241.1;
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